

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:26 ; Search time 41.2414 Seconds
(without alignments)
594.503 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009
Sequence: 1 CTCVPPHPQAFPCNSDLVIR.....ACLPREPGLCTWQSLRSQIA 184

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Sequenced: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
8: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
11: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
17: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1009	100.0	184	23	AAU99875 Human tissue inhib
2	1009	100.0	207	7	AAU99875 Sequence of tissue
3	1009	100.0	207	7	AAU99875 Sequence of tissue
4	1009	100.0	207	7	AAU99875 Sequence of tissue
5	1009	100.0	207	18	AAU99875 Sequence of tissue
6	1009	100.0	207	20	AAU99875 Sequence of tissue
7	1009	100.0	207	21	AAU99875 Sequence of tissue
8	1009	100.0	580	23	AAU99882 Human TIMP-1 prote
9	1009	100.0	580	23	AAU99882 Human TIMP-1 prote
10	1006	99.7	207	7	AAU99889 Sequence of a glibb

11	1005	99.6	207	22	AAU99875 Human secreted pro
12	1004	99.5	207	22	AAU99875 Human polypeptide,
13	989	98.0	207	16	AAU99875 Human tissue inhib
14	928	92.0	204	23	AAU99875 Human ovarian anti
15	893	88.5	207	16	AAU99875 Cattle tissue inh
16	850	84.2	207	16	AAU99875 Pig tissue inhib
17	807.5	80.0	206	16	AAU99875 Rabbit tissue inh
18	761.5	75.5	205	16	AAU99875 Mouse tissue inh
19	703.5	69.7	207	16	AAU99875 Human tissue inh
20	691	68.5	128	23	AAU99875 Human TIMP-1-128 p
21	682	67.6	127	23	AAU99875 Human TIMP-1-127 p
22	682	67.6	127	23	AAU99875 Human TIMP-1-127 p
23	682	67.6	127	23	AAU99875 Human TIMP-1-127 p
24	667.5	66.2	183	21	AAU99875 Human cancer assoc
25	615.5	61.0	212	23	AAU99875 Human ovarian anti
26	604	59.9	162	23	AAU99875 Human ovarian anti
27	386	38.3	192	11	AAU99875 Metalloproteinase
28	382.5	37.9	194	23	AAU99875 Rat matrix metallo
29	382.5	37.9	194	23	AAU99875 Chicken ischaemic co
30	381.5	37.8	212	16	AAU99875 Human TIMP-3
31	380	37.7	193	23	AAU99875 Human TIMP-3
32	377.5	37.4	188	18	AAU99875 Human TIMP-3
33	377.5	37.4	194	21	AAU99875 Human TIMP-3
34	377.5	37.4	198	16	AAU99875 Human TIMP-3
35	377.5	37.4	206	16	AAU99875 Human TIMP-3
36	377.5	37.4	211	16	AAU99875 Human TIMP-3
37	377.5	37.4	211	16	AAU99875 Human TIMP-3
38	377.5	37.4	211	18	AAU99875 Human TIMP-3
39	377.5	37.4	211	20	AAU99875 Human TIMP-3
40	377.5	37.4	211	21	AAU99875 Human TIMP-3
41	377.5	37.4	220	11	AAU99875 Human TIMP-3
42	377.5	37.4	220	15	AAU99875 Human TIMP-3
43	377.5	37.4	220	16	AAU99875 Human TIMP-3
44	377.5	37.4	220	19	AAU99875 Human TIMP-3
45	377.5	37.4	220	20	AAU99875 Human TIMP-3

ALIGNMENTS

RESULT 1
AAU99875
ID AAU99875 standard; Protein; 184 AA.
AC AAU99875;
DT 07-OCT-2002 (first entry)
XX Human tissue inhibitor of metalloproteases (TIMP).
DE
XX Tissue inhibitor of metalloproteases; human; TIMP; protease inhibitor;
KW malacia; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
XX
XX Homo sapiens.
OS
XX
XX WO200250287-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US49256.
XX
XX 18-DEC-2001; 2000US-256699P.
XX
XX 20-NOV-2001; 2001US-331966P.
XX
XX (ARRI-) ARRIYA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX

DR WPI; 2002-500631/53.
DR N-PSDB; ABK88017.
XX
XX
XX Novel fusion protein useful for inhibiting protease activity associated
PT with a disorder such as emphysema, asthma, comprises a first protease
PT inhibitor comprising alpha 1-antitrypsin and a second protease
PT inhibitor -
XX
XX Disclosure; Page 37; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally
CC active portion and a second protease inhibitor or its functionally
CC active protein. The fusion proteins of the invention may act as an
CC inhibitor of protease activity. The fusion protein of the invention
CC is useful for inhibiting protease activity associated with a disorder
CC such as emphysema, asthma, chronic obstructive pulmonary disease,
CC cystic fibrosis, otitis media, otitis externa or HIV infection, or
CC for treating an individual suffering from or at risk for a disease or
CC disorder involving unwanted protease activity. The proteins are useful
CC for treating dermatological diseases such as atopic dermatitis, eczema
CC and psoriasis, in inflammatory responses to viral infection, and for
CC treating herpes infection, corneal or epidermal ulceration, chronic
CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
CC tumour metastasis and tumour angiogenesis, gastric ulceration,
CC osteoporosis, Peget's disease, glomerulonephritis, scleroderma, malaria,
CC bacterial infection, Alzheimer's disease, hypertension and muscular
CC dystrophy. The present sequence represents the human tissue inhibitor
CC of metalloproteases used to create the fusion protein of the invention.
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 1009; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTQTLVQRYEIKMTKMYKGFQALGDAADIRF 60
Db 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTQTLVQRYEIKMTKMYKGFQALGDAADIRF 60
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120
Qy 121 TVGCECTVFPCLSIKQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Db 121 TVGCECTVFPCLSIKQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Qy 181 SQIA 184
Db 181 SQIA 184

RESULT 2
AAP60786
ID AAP60786 standard; Protein; 207 AA.
XX
XX AAP60786;
XX
XX 08-AUG-1991 (first entry)
XX
XX Sequence of tissue inhibitor of metalloproteinase (TIMP).
XX
XX Connective tissue; extracellular matrix.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= signal
FT Protein 24..207
FT Modified-site 53..55
FT /label= potential N-glycosylation site

FT Modified-site 101..103
FT /label= as above
XX
XX GB2169295-A.
XX
XX 09-JUL-1986.
XX
XX 06-JAN-1986; 86GB-0000199.
XX
XX 01-NOV-1985; 85GB-0026951.
XX 07-JAN-1985; 85GB-0000341.
XX 06-JAN-1986; 86GB-0000199.
XX 07-JAN-1985; 85GB-0500341.
XX 05-OCT-1983; 83BE-0897924.
XX (CELL-) CELLTech LTD.
XX
XX Harris TUR, Reynolds JJ, Docherty AJP, Murphy G;
XX
XX WPI; 1986-177873/28.
XX N-PSDB; AAN60538.
XX
XX Prodn. of metallo-proteinase inhibitors - by recombinant DNA
PT techniques
XX
XX Disclosure; Fig 3; 16pp; English.
XX
XX A gene with residues 64-684 of AAN60538 is claimed. AAN60538 was
CC isolated from human a foetal diploid lung cells (ATCC CLL153) cDNA
CC library using AAN60539.
XX
SQ Sequence 207 AA;

Query Match 100.0%; Score 1009; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.2e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTQTLVQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTQTLVQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCECTVFPCLSIKQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Db 144 TVGCECTVFPCLSIKQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203
Qy 181 SQIA 184
Db 204 SQIA 207

RESULT 3
AAP60275
ID AAP60275 standard; Protein; 207 AA.
XX
XX AAP60275;
XX
XX 03-OCT-2002 (updated)
XX 08-AUG-1991 (first entry)
XX
XX Sequence of human natural inhibitor of collagenases (NIC).
XX
XX Metallo-proteinase inhibitor; wound healing; emphysema;
XX rheumatoid arthritis therapy; ulceration; tumour metastasis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= signal

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FT Protein 24..207
FT /note= "claimed"
FT Modified-site 53..55
FT /note= "potential glycosylation site"
FT Modified-site 101..103
FT /note= "potential glycosylation site"
XX
XX EPI89784-A.
XX
XX PD 06-AUG-1986.
XX
XX PF 16-JAN-1986; 86EP-0100482.
XX
XX PR 18-JAN-1985; 85US-0692808.
XX
XX PA (SEAR ) SEARLE G D & CO.
XX
XX PI Galloway WA, Clissold PM, McCullagh KG;
XX
XX DR MPI; 1986-205910/32.
XX N-PSDB; AAN60277.
XX
PT New human natural inhibitor of collagenase - for treating e.g.
PT rheumatoid arthritis or ulceration, and new DNA sequences coding
PT for it
XX
XX PS Disclosure; Fig 2; 51pp; English.
XX
XX CC The patentors claim the AA SQ of human NIC, DNA sequences coding for
XX CC NIC, and its RNA analogues and plasmids contg. this DNA. NIC
XX CC inhibits the activity of metallo-proteinases, esp. of collagenase,
XX CC proteoglycanase, gelatinase or a leucocyte, macrophage or tumour
XX CC cell metallo-proteinase.
XX CC (updated on 03-OCT-2002 to add missing OS field.)
XX
XX SQ Sequence 207 AA;

Query Match 100.0%; Score 1009; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.2e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYQREIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYQREIKMTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 120
D 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180
DB 144 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 203
QY 181 SQIA 184
DB 204 SQIA 207

RESULT 4
AAP60592
ID AAP60592 standard; Protein; 207 AA.
XX
XX AC AAP60592;
XX
XX DT 13-AUG-1991 (first entry)
XX
XX DE Sequence of a human protein having erythroid potentiating
XX DE activity (EPA).
XX
XX KW Erythroid precursor growth; anaemia therapy.
XX
XX OS Homo sapiens.
XX

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PN W08602100-A.
XX
XX PD 10-APR-1986.
XX
XX PF 01-OCT-1985; 85WO-5001900.
XX
XX PR 01-OCT-1984; 84US-0656590.
XX
XX PA (SANO ) SANDOZ LTD.
XX PA (REGC ) REGENTS OF UNIV OF CALIF.
XX
XX PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
XX
XX DR MPI; 1986-106663/16.
XX N-PSDB; AAN60494.
XX
XX PT Vectors contg. gene for protein having erythroid potentiating
XX PT activity - used for producing protein to stimulate growth and
XX PT formation of erythroid cells
XX
XX PS Disclosure; Fig 4; 59pp; English.
XX
XX CC The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)
XX CC and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a
XX CC biological activity of at least about 1,000,000 units per mg of
XX CC protein and has an apparent molecular weight of about 28,000 daltons.
XX
XX SQ Sequence 207 AA;

Query Match 100.0%; Score 1009; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.2e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYQREIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPHPQTAFNCSDLVIRAKFVGTPEVNOTTLVYQREIKMTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGDLHITTCSPVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180
DB 144 TVGCECTVPFCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 203
QY 181 SQIA 184
DB 204 SQIA 207

RESULT 5
AAN60309
ID AAN60309 standard; Protein; 207 AA.
XX
XX AC AAN60309;
XX
XX DT 29-JAN-1998 (first entry)
XX
XX DE Human TIMP-1.
XX
XX KW TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;
XX KW cancer progression; TIMP-1.
XX
XX OS Homo sapiens.
XX
XX PD 09-SEP-1997.
XX
XX PF 29-FEB-1996; 96JP-0067484.
XX
XX PR 29-FEB-1996; 96JP-0067484.
XX

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PA (FUJII) FUJII PHARM IND CO LTD.
XX WPI; 1997-498341/46.
DR N-PSDB; AAT92631.
XX
XX Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used in
PT diagnosis of TIMP-3 mediated diseases, especially the detection of
PT malignant tumour cells
XX
XX Example 12; Page 33-34; 37pp; Japanese.
PS
CC This sequence represents the human TIMP-1 protein. This sequence was
CC used to test the specificity of the monoclonal antibody (MAB) of the
CC invention. The MAB of the invention reacts specifically with human
CC TIMP-3 (see AAW30308), by specific recognition of the TIMP-3 fragments
CC represented by AAW30305-W30307. The MAB can be used in the study or
CC diagnosis of TIMP-3-mediated diseases, particularly for the detection of
CC malignant tumour cells, or the diagnosis of progressiveness of cancers.
CC They can also be used in establishing an immunoassay for TIMP-3 or in
CC purification of TIMP-3. The transformed cells can be used for producing
CC TIMP-3 or its equivalent proteins on a large scale. The immunoassay
CC method for TIMP-3 the MABs is simple, highly reproducible and highly
CC sensitive.
XX
XX Sequence 207 AA;
SQ
Query Match 100.0%; Score 1009; DB 18; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.2e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 60
DB 24 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 143
QY 121 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 180
DB 144 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 203
QY 181 SQIA 184
DB 204 SQIA 207
RESULT 6
ID AAY08933 standard; Protein; 207 AA.
XX
XX AAY08933;
AC
XX
XX 19-AUG-1999 (first entry)
DT
XX
XX Human TIMP-1 protein.
DE
XX
XX TIMP-4; tissue inhibitor of metalloprotease; human; antibody; diagnosis;
KW treatment; metastasis; neoplastic cell; angiogenesis; tumour; cervical;
KW uterine; pancreatic; colon; intestinal carcinoma; pregnancy; ulcer;
KW osteoarthritis; pulmonary emphysema; periodontal disease; corneal;
KW rheumatoid arthritis; diabetic ulcer; lesion; TIMP-4.
XX
XX Homo sapiens.
OS
XX
XX US5914392-A.
PN
XX
XX 22-JUN-1999.
PD
XX
XX 07-JUL-1998; 98US-0111070.
PF
XX
XX 18-JAN-1996; 96US-0588163.
PR
XX 27-JUN-1997; 97US-0884073.
PR

PR 07-JUL-1998; 98US-0111070.
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX
XX Hawkins PR, Murry LE;
PI
XX
XX WPI; 1999-384187/32.
DR
XX
XX Anti-tissue inhibitor metalloproteinase antibodies useful for
PT treating and diagnosing cancer
PT
XX
XX Disclosure; Fig 4; 26pp; English.
PS
XX
XX This invention describes a novel method for the production of antibodies
CC specific for the human tissue inhibitors of metalloproteinase 4, TIMP-4.
CC The anti-TIMP-4 antibodies may be used to treat, prevent or diagnose
CC metastasis of neoplastic cells, angiogenesis and growth tumours such as
CC cervical, uterine, pancreatic, colon or intestinal carcinomas, pregnancy,
CC osteoarthritis, pulmonary emphysema, periodontal disease, rheumatoid
CC arthritis, corneal or diabetic ulcers or ulcers and lesions caused by
CC microorganisms. This sequence represents TIMP-4 which is used to
CC describe the method of the invention.
XX
XX Sequence 207 AA;
SQ
Query Match 100.0%; Score 1009; DB 20; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.2e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 60
DB 24 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 143
QY 121 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 180
DB 144 TVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLGSEKGFQSRHLACLPREPGLCTWQSLR 203
QY 181 SQIA 184
DB 204 SQIA 207
RESULT 7
ID AAB19073 standard; protein; 207 AA.
XX
XX AAB19073;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Inhibitor of tissue metalloproteinase designated TIMP-1.
DE
XX
XX Tissue metalloproteinase inhibitor; TIMP; metalloproteinase; gelatinase;
KW metastasis; cancer.
KW
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /note= "signal peptide"
FT 24..207
FT Protein /note= "mature protein"
FT
XX
XX EP1041083-A1.
PN
XX
XX 04-OCT-2000.
PD
XX
XX 03-APR-2000; 2000EP-0107041.
PF
XX

PR 01-APR-1999; 99JP-0095142.
 XX (ORIY) ORIENTAL YEAST CO LTD.
 XX Miyazaki K, Higashi S;
 XX WPI: 2000-603818/58.
 DR
 XX New modified tissue inhibitor of metalloproteinases, useful for
 PT manufacturing compositions for inhibiting metastasis of cancer and
 PT vascularisation and for preventing or treating diseases associated with
 PT these, e.g. brain tumor
 XX
 PS Disclosure; Page 12-13; 25pp; English.
 XX
 CC The present sequence represents an inhibitor of tissue metalloproteinase,
 CC designated TIMP. The specification describes modified forms of TIMP,
 CC where the amino-terminal alpha-amino group is modified with an electron
 CC accepting group to substantially lose the ability to bind to a
 CC metalloproteinase. Modified TIMP-2 prevents an accumulation of active
 CC gelatinase. A on the cell surface, and can inhibit the activation of
 CC precursor matrix metalloproteinases. The modified TIMP-2 and the
 CC compositions comprising TIMP-2 are useful for inhibiting metastasis of
 CC cancer and vascularisation. It is also used for treating diseases
 CC associated with them. Specifically, these are useful for preventing or
 CC treating metastasis of cancer of the stomach, colon, lung, head and
 CC neck, brain tumor, breast, thyroid, prostate, ovary or pancreas, or
 CC vascularisation or other conditions associated with these.
 XX
 SQ Sequence 207 AA;
 Query Match 100.0%; Score 1009; DB 21; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2,2e-99;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVPHQQTAFNCSDLVIRAKFVGTPEVNOITLYORYEIKMTWKYKGFQALGDAADIRF 60
 DB 24 CTCVPHQQTAFNCSDLVIRAKFVGTPEVNOITLYORYEIKMTWKYKGFQALGDAADIRF 83
 QY 61 VYTPAMEVCGYFPHSHNRSEELIAGKLDGDLHITTCSPVAPWNSISLQORRGFTTXY 120
 DB 84 VYTPAMEVCGYFPHSHNRSEELIAGKLDGDLHITTCSPVAPWNSISLQORRGFTTXY 143
 QY 121 TVGSECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWOSLR 180
 DB 144 TVGSECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWOSLR 203
 QY 181 SQIA 184
 DB 204 SQIA 207
 RESULT 8
 AAU99882
 ID AAU99882 standard; Protein, 580 AA.
 XX AAU99882;
 AC
 XX 07-OCT-2002 (first entry)
 DT
 XX
 DE TAP1 fusion protein.
 XX
 XX TAP1; Alzheimer's disease; tumour angiogenesis;
 KM malaria; emphysema; asthma; chronic obstructive pulmonary disease;
 KM cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
 KM human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
 KM herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
 KM tumour metastasis; osteoporosis; Paget's disease; scleroderma;
 KM glomerulonephritis; hypertension.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Region 2..185
 FT /note= "Human TIMP-1 amino acids 1-184"
 FT Region 186
 FT /note= "Linker methionine"
 FT Region 187..580
 FT /note= "Amino acids 1-394 of human AAT"
 XX
 XX WO200250287-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 18-DEC-2001; 2001WO-US49256.
 XX
 XX 18-DEC-2000; 2000US-256699P.
 XX 20-NOV-2001; 2001US-331966P.
 XX
 XX (ARRI-) ARRIYA PHARM INC.
 XX
 XX Barr PJ, Gibson HL, Pemberton P;
 XX
 XX WPI: 2002-500631/53.
 XX N-PSDB; ABK88023.
 XX
 XX Novel fusion protein useful for inhibiting protease activity associated
 XX with a disorder such as emphysema, asthma, comprises a first protease
 XX inhibitor comprising alpha 1-antitrypsin and a second protease
 XX inhibitor -
 XX
 XX Example 1; Page 79-82; 134pp; English.
 XX
 XX This invention relates to a novel fusion protein comprising a first
 XX protease inhibitor comprising an alpha 1-antitrypsin or its functionally
 XX active portion and a second protease inhibitor or its functionally
 XX active portion. The fusion proteins of the invention may act as an
 XX inhibitor of protease activity. The fusion protein of the invention
 XX is useful for inhibiting protease activity associated with a disorder
 XX such as emphysema, asthma, chronic obstructive pulmonary disease,
 XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
 XX for treating an individual suffering from or at risk for a disease or
 XX disorder involving unwanted protease activity. The proteins are useful
 XX for treating dermatological diseases such as atopic dermatitis, eczema
 XX and psoriasis, in inflammatory responses to viral infection, and for
 XX treating herpes infection, corneal or epidermal ulceration, chronic
 XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
 XX tumour metastasis and tumour angiogenesis, gastric ulceration,
 XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
 XX bacterial infection, Alzheimer's disease, hypertension and muscular
 XX dystrophy. The present sequence represents the TAP1 fusion protein of
 XX the invention.
 XX
 SQ Sequence 580 AA;
 Query Match 100.0%; Score 1009; DB 23; Length 580;
 Best Local Similarity 100.0%; Pred. No. 8,3e-99;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVPHQQTAFNCSDLVIRAKFVGTPEVNOITLYORYEIKMTWKYKGFQALGDAADIRF 60
 DB 2 CTCVPHQQTAFNCSDLVIRAKFVGTPEVNOITLYORYEIKMTWKYKGFQALGDAADIRF 61
 QY 61 VYTPAMEVCGYFPHSHNRSEELIAGKLDGDLHITTCSPVAPWNSISLQORRGFTTXY 120
 DB 62 VYTPAMEVCGYFPHSHNRSEELIAGKLDGDLHITTCSPVAPWNSISLQORRGFTTXY 121
 QY 121 TVGSECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWOSLR 180
 DB 122 TVGSECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWOSLR 181
 QY 181 SQIA 184
 DB 182 SQIA 185

RESULT 9
AAU99889
ID AAU99889 standard; Protein; 580 AA.
XX
AC AAU99889;
XX
DT 07-OCT-2002 (first entry)
XX
DE rTAP1 fusion protein.
XX
KW rTAP1; Alzheimer's disease; tumour angiogenesis;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
KW glomerulonephritis; hypertension.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 2..395
FT Region /note= "Human AAT amino acids 1-394"
FT Region 396
FT Region /note= "Linker methionine"
FT Region 397..580
FT Region /note= "Amino acids 1-184 of human TIMP-1"
XX
PN WO200250287-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-US49256.
XX
PR 18-DEC-2000; 2000US-256699P.
PR 20-NOV-2001; 2001US-331966P.
XX
PA (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX WPI; 2002-500631/53.
DR N-PSDB; ASK88026.
XX
PT Novel fusion protein useful for inhibiting protease activity associated
PT with a disorder such as emphysema, asthma, comprises a first protease
PT inhibitor comprising alpha 1-antitrypsin and a second protease
PT inhibitor -
XX
XX Example 3; Page 94; 134pp; English.
XX
CC This invention relates to a novel fusion protein comprising a first
CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally
CC active portion and a second protease inhibitor or its functionally
CC active portion. The fusion proteins of the invention may act as an
CC inhibitor of protease activity. The fusion protein of the invention
CC is useful for inhibiting protease activity associated with a disorder
CC such as emphysema, asthma, chronic obstructive pulmonary disease,
CC cystic fibrosis, otitis media, otitis externa or HIV infection, or
CC for treating an individual suffering from or at risk for a disease or
CC disorder involving unwanted protease activity. The proteins are useful
CC for treating dermatological diseases such as atopic dermatitis, eczema
CC and psoriasis, in inflammatory responses to viral infection, and for
CC treating herpes infection, corneal or epidermal ulceration, chronic
CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
CC tumour metastasis and tumour angiogenesis, gastric ulceration,
CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma,
CC bacterial infection, Alzheimer's disease, hypertension and muscular
CC dystrophy. The present sequence represents the rTAP1 fusion protein of
CC the invention.

SQ Sequence 580 AA;
Query Match 100.0%; Score 1009; DB 23; Length 580;
Best Local Similarity 100.0%; Pred. No. 8.3e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 397 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 456
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 120
Db 457 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAORRGFTKTY 516
Qy 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 180
Db 517 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGEKGFQSRHLACLPREPGLCTWQSLR 576
Qy 181 SQIA 184
Db 577 SQIA 580
RESULT 10
AAP60593
ID AAP60593 standard; Protein; 207 AA.
XX
AC AAP60593;
XX
DT 13-AUG-1991 (first entry)
XX
DE Sequence of a gibbon protein having erythroid potentiating
DE activity (EPA).
XX
KW Erythroid precursor growth; anaemia therapy.
XX
OS Gibbon.
XX
PN WO8602100-A.
XX
PD 10-APR-1986.
XX
PF 01-OCT-1985; 85WO-5001900.
XX
PR 01-OCT-1984; 84US-0656590.
XX
PA (SANO) SANDOZ LTD.
PA (REGC) REGENTS OF UNIV OF CALIFO.
XX
PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
XX
XX WPI; 1986-106663/16.
DR N-PSDB; AAN60495.
XX
PT Vectors contg. gene for protein having erythroid potentiating
PT activity - used for producing protein to stimulate growth and
PT formation of erythroid cells
XX
PS Disclosure; Fig 5; 59pp; English.
XX
CC The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)
CC and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a
CC biological activity of at least about 1,000,000 units per mg of
CC protein and has an apparent molecular weight of about 28,000 daltons.
XX
SQ Sequence 207 AA;
Query Match 99.7%; Score 1006; DB 7; Length 207;
Best Local Similarity 99.5%; Pred. No. 4.6e-99;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNOITLYQRYEIKMTKMYKGFQALGDAADIRF 60
|||||

Db 24 CTCVPHQPTAFCSNDIVAKAFVGTPEVNQTTLYQRYEIKMTKMYKGFOLGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Db 144 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203
QY 181 SOIA 184
Db 204 SOIA 207

RESULT 11

AAG89171
ID AAG89171 standard; Protein; 207 AA.

XX AAG89171;

DT 11-SEP-2001 (first entry)

DE Human secreted protein; SEQ ID NO: 291.

XX Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;

XX GENSET.

XX Homo sapiens.

XX WO200142451-A2.

XX 14-JUN-2001.

PF 07-DEC-2000; 2000MO-IB01938.

PR 08-DEC-1999; 99US-0169629.

PR 06-MAR-2000; 2000US-0187470.

XX (GENSET) GENSET.

XX Dumas Mline Edwards J, Bougueleret L, Jobert S;

DR WPI; 2001-367870/38.

XX N-PSDB; AAH64774.

PS Claim 21; Page 825; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding
XX potentially secreted proteins. The nucleic acids and the polypeptides
XX they encode may be used in the prevention, treatment and diagnosis of
XX diseases associated with inappropriate GENSET gene expression. For
XX example, they be used to treat disorders associated with decreased
XX GENSET gene expression by rectifying mutations or deletions in a
XX patient's genome that affect the activity of GENSET or by supplementing
XX the patient's own production of GENSET polypeptides. Conversely,
XX antisense nucleic acid molecules may be administered to down regulate
XX GENSET expression by binding with the cells' own genes and preventing
XX their expression. The sense and antisense nucleic acids may also be
XX used as DNA probes in diagnostic assays to detect and quantitate the
XX presence of similar nucleic acid sequences in samples, and hence to
XX determine which patients may be in need of restorative therapy.
XX The GENSET polypeptides may be used as antigens in the production of
XX antibodies and in assays to identify modulators (agonists and
XX antagonists) of GENSET polypeptide expression and activity. The
XX present sequence is a GENSET polypeptide of the invention.

XX Sequence 207 AA;

Query Match 99.6%; Score 1005; DB 22; Length 207;
Best Local Similarity 99.5%; Pred. No. 5.8e-99;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTCVPHQPTAFCSNDIVAKAFVGTPEVNQTTLYQRYEIKMTKMYKGFOLGDAADIRF 60
Db 24 CTCVPHQPTAFCSNDIVAKAFVGTPEVNQTTLYQRYEIKMTKMYKGFOLGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180
Db 144 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203
QY 181 SOIA 184
Db 204 SOIA 207

RESULT 12

AAM93377
ID AAM93377 standard; Protein; 207 AA.

XX AAM93377;

DT 06-NOV-2001 (first entry)

DE Human polypeptide; SEQ ID NO: 2953.

XX Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2001-524255/58.

XX N-PSDB; AAK94297.

PS Claim 8; SEQ ID NO 2953; 1380bp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesised by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence is a polypeptide
XX encoded by a full length human cDNA of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 207 AA;

Query Match 99.5%; Score 1004; DB 22; Length 207;
Best Local Similarity 99.5%; Pred. No. 7.4e-99;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCVPHPTAFCSNLDLIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPHPTAFCSNLDLIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

QY 61 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNSLSLAQRGGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNSLSLAQRGGFTKTY 143

QY 121 TVGCECTVFPCLSPCKLQSGTHCLWTDOLQSGSEKGFQSRHLACLPREPGLCTWQSUR 180
DB 144 TVGCECTVFPCLSPCKLQSGTHCLWTDOLQSGSEKGFQSRHLACLPREPGLCTWQSUR 203

QY 181 SQIA 184
DB 204 SQIA 207

RESULT 13
AAR65005
ID AAR65005 standard; Protein; 207 AA.
XX AC AAR65005;
XX DT 23-OCT-1995 (first entry)
XX DE Human tissue inhibitor of metalloproteinase (TIMP-1).
XX KW Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;
XX KW prophylaxis.
XX OS Homo sapiens.
XX PN WO9505478-A.
XX PD 23-FEB-1995.
XX PF 12-AUG-1994; 94WO-US09188.
XX PR 12-AUG-1993; 93US-0105263.
XX PR 13-DEC-1993; 93US-0167463.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Hawkes SP, Kishnani NS, Yang T;
XX DR WPI; 1995-098775/13.
XX PT New human tissue inhibitor of metalloproteinase-3 - used to
XX PT develop prods. for diagnosis, therapy or prophylaxis of
XX PT conditions with unwanted matrix metalloproteinase activity.
XX PS Disclosure; Fig 6A-B; 87pp; English.
XX CC The protein sequence of the human TIMP-1 is compared with those
XX CC from pig, cattle, rabbit and mouse TIMP-1, human, mouse and cattle
XX CC TIMP-2 and chicken (Ch) and mouse TIMP-3. A probe based on the
XX CC CHIMP-3 amino acid sequence (AAR65000) is used to isolate DNA
XX CC encoding human TIMP-3 from a human cDNA library. Human TIMP-3
XX CC can be used for the diagnosis, therapy or prophylaxis of
XX CC conditions characterized by excess or unwanted matrix
XX CC metalloproteinase activity, e.g. neoplasias, tumor metastasis,
XX CC inflammatory disorders such as rheumatoid arthritis, ulcerations,
XX CC reaction to infection, periodontal disease or osteoporosis. It can
XX CC also be used in drug screening/design.

SQ Sequence 207 AA;

Query Match 98.0%; Score 989; DB 16; Length 207;
Best Local Similarity 98.4%; Pred. No. 3e-97;

Matches 181; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCVPHPTAFCSNLDLIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPHPTAFCSNLDLIRAKFVGTPVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

QY 61 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNSLSLAQRGGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWNSLSLAQRGGFTKTY 143

QY 121 TVGCECTVFPCLSPCKLQSGTHCLWTDOLQSGSEKGFQSRHLACLPREPGLCTWQSUR 180
DB 144 TVGCECTVFPCLSPCKLQSGTHCLWTDOLQSGSEKGFQSRHLACLPREPGLCTWQSUR 203

QY 181 SQIA 184
DB 204 SQIA 207

RESULT 14
ABP42206
ID ABP42206 standard; Protein; 204 AA.
XX AC ABP42206;
XX DT 22-AUG-2002 (first entry)
XX DE Human ovarian antigen HCOQ079, SEQ ID NO:3338.
XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
XX KW inflammatory condition; immune disorder; blood disorder;
XX KW cardiovascular disorder; respiratory disorder; neurological disorder;
XX KW gastrointestinal disorder; urinary system disorder; drug screening;
XX KW gene therapy; chromosome mapping; forensic analysis;
XX KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX KW antiinflammatory; gynaecological; reproductive.
XX OS Homo sapiens.
XX PN WO200200677-A1.
XX PD 03-JAN-2002.
XX PF 07-JUN-2001; 2001WO-US18569.
XX PR 07-JUN-2000; 2000US-209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-147878/19.
XX DR N-PSDB; ABQ55283.
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX PT useful in the prevention, treatment and diagnosis of cancer (e.g.
XX PT ovarian cancer), immune disorders, cardiovascular disorders and
XX PT neurological diseases -
XX PS Claim 11; SEQ ID NO 3338; 2922pp; English.
XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX CC encompasses polypeptides 90% identical and polynucleotides 95% identical
XX CC to the sequences of the invention. The invention additionally relates to
XX CC recombinant vectors and host cells comprising human ovarian antigen
XX CC polynucleotides, antibodies against human ovarian antigens, and the use
XX CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX CC treating, prognosing or preventing various ovary and/or breast-related
XX CC disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPD
XX at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 204 AA;

Query Match 92.0%; Score 928; DB 23; Length 204;
Best Local Similarity 99.4%; Pred. No. 9.4e-91;
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFNCNSDVIYRAKFGVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDADIRF 60
DB 22 CTCVPPHPQTAFNCNSDVIYRAKFGVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDADIRF 81
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 120
DB 82 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 141
QY 121 TVGCECTVPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPRE 170
DB 142 TVGCECTVPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPRE 191

RESULT 15

ID AAR65003 standard; Protein; 207 AA.

AC AAR65003;

DT 23-OCT-1995 (first entry)

DB Cattle tissue inhibitor of metalloproteinase (TIMP-1).

KM Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;
prophylaxis.

OS Bos primigenius taurus.

PN M09505478-A.

PD 23-FEB-1995.

PF 12-AUG-1994; 94WO-US09188.

PR 12-AUG-1993; 93US-0105263.

PR 13-DEC-1993; 93US-0167463.

PA (REGC) UNIV CALIFORNIA.

PI Hawkes SP, Kishnani NS, Yang T;

WPI; 1995-098775/13.

XX New human tissue inhibitor of metallo:proteinase-3 - used to
XX develop prods. for diagnosis, therapy or prophylaxis of
XX conditions with unwanted matrix metallo:proteinase activity.
PT

XX Disclosure: Fig 6A-B; 87pp; English.

PS The protein sequence of the cattle TIMP-1 is compared with those
XX from pig, human, rabbit and mouse TIMP-1, human, mouse and cattle
XX TIMP-2 and chicken (Ch) and mouse TIMP-3. A probe based on the
XX ChIMP-3 amino acid sequence (AAR65000) is used to isolate DNA
XX encoding human TIMP-3 from a human cDNA library. Human TIMP-3
XX can be used for the diagnosis, therapy or prophylaxis of
XX conditions characterized by excess or unwanted matrix
XX metalloproteinase activity, e.g. neoplasias, tumor metastasis,
XX inflammatory disorders such as rheumatoid arthritis, ulcerations,
XX reaction to infection, periodontal disease or osteoporosis. It can
XX also be used in drug screening/design.

SQ Sequence 207 AA;

Query Match 88.5%; Score 893; DB 16; Length 207;
Best Local Similarity 87.0%; Pred. No. 5.2e-87;
Matches 160; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFNCNSDVIYRAKFGVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPPHPQTAFNCNSDVIYRAKFGVGTAEVNETALYQRYEIKMTKMYKGFQALRDADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 120
DB 84 IYTPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPREGLCTWQSLR 180
DB 144 AAGCECTVPCLSIIPCKLQSGTHCLMTDQLLQSGSEKGFQSHLACLPREGLCTWQSLR 203
QY 181 SQIA 184
DB 204 AQMA 207

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Job time : 43.2414 secs

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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 14.5931 Seconds
(without alignments)
370.985 Million cell updates/sec

Title: US-09-452-817-1

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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Sequenced: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	100.0	184	US-09-452-817-1	Sequence 1, Appli
2	1009	100.0	207	US-08-588-163-5	Sequence 5, Appli
3	1009	100.0	207	US-09-111-070-5	Sequence 5, Appli
4	1009	100.0	207	US-08-849-764C-5	Sequence 5, Appli
5	1009	100.0	207	US-09-262-087-5	Sequence 5, Appli
6	1009	100.0	207	US-08-463-261B-11	Sequence 11, Appli
7	579	57.4	106	US-09-452-817-2	Sequence 2, Appli
8	377.5	37.4	211	US-08-588-163-4	Sequence 4, Appli
9	377.5	37.4	220	US-09-111-070-4	Sequence 4, Appli
10	377.5	37.4	220	US-08-588-163-3	Sequence 3, Appli
11	377.5	37.4	220	US-09-111-070-3	Sequence 3, Appli
12	372	36.9	210	US-08-849-764C-4	Sequence 4, Appli
13	372	36.9	210	US-09-262-087-4	Sequence 4, Appli
14	372	36.9	210	US-08-463-261B-10	Sequence 10, Appli
15	369.5	36.6	218	US-08-849-764C-3	Sequence 3, Appli
16	369.5	36.6	218	US-09-262-087-3	Sequence 3, Appli
17	369.5	36.6	218	US-08-463-261B-9	Sequence 9, Appli
18	351	34.8	224	US-08-588-163-2	Sequence 2, Appli
19	351	34.8	224	US-09-111-070-2	Sequence 2, Appli
20	351	34.8	224	US-08-849-764C-2	Sequence 2, Appli
21	351	34.8	224	US-09-262-087-2	Sequence 2, Appli
22	351	34.8	224	US-08-463-261B-2	Sequence 2, Appli
23	351	34.8	224	PCT-US94-14498A-2	Sequence 2, Appli
24	124	12.3	25	US-08-474-696A-2	Sequence 2, Appli
25	105	10.4	22	US-08-474-696A-5	Sequence 5, Appli
26	105	10.4	22	US-08-474-696A-6	Sequence 6, Appli
27	105	10.4	25	US-08-474-696A-4	Sequence 4, Appli

28	88.5	8.8	512	1	US-07-779-890-4	Sequence 4, Appli
29	88.5	8.8	512	1	US-07-779-890-4	Sequence 4, Appli
30	88.5	8.8	512	2	US-09-008-962-4	Sequence 4, Appli
31	88.5	8.8	512	2	US-08-675-507-4	Sequence 4, Appli
32	88.5	8.8	512	3	US-09-213-205-4	Sequence 4, Appli
33	88.5	8.8	512	3	PCT-US93-05640-4	Sequence 4, Appli
34	78	7.7	535	2	US-08-633-879C-4	Sequence 4, Appli
35	77	7.6	16	2	US-08-480-190-134	Sequence 134, App
36	77	7.6	16	2	US-08-488-379-134	Sequence 134, App
37	77	7.6	16	5	PCT-US93-07545-134	Sequence 134, App
38	73	7.2	537	2	US-08-633-879C-2	Sequence 2, Appli
39	72.5	7.2	425	1	US-08-414-926A-15	Sequence 15, Appli
40	72.5	7.2	425	2	US-08-926-922-15	Sequence 15, Appli
41	72.5	7.2	425	3	US-09-253-682-15	Sequence 15, Appli
42	72.5	7.2	425	4	US-09-527-657-15	Sequence 15, Appli
43	72	7.1	15	2	US-08-480-190-135	Sequence 135, App
44	72	7.1	15	2	US-08-480-190-247	Sequence 247, App
45	72	7.1	15	2	US-08-488-379-135	Sequence 135, App

ALIGNMENTS

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RESULT 1
US-09-452-817-1
; Sequence 1, Application US/09452817
; Patent No. 6342374
; GENERAL INFORMATION:
; APPLICANT: Carmichael, David F
; APPLICANT: Anderson, David C
; APPLICANT: Stricklin, George P
; APPLICANT: Welgus, Howard G
; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
; TITLE OF INVENTION: For Using Same And Recombinant DNA Method For
; FILE REFERENCE: Serial No. 6342374 09/452,817
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/452,817
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/050,739
; PRIOR FILING DATE: 1993-04-21
; PRIOR APPLICATION NUMBER: 07/853,018
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: 07/517,475
; PRIOR FILING DATE: 1990-05-01
; PRIOR APPLICATION NUMBER: 07/320,923
; PRIOR FILING DATE: 1989-03-08
; PRIOR APPLICATION NUMBER: 06/784,319
; PRIOR FILING DATE: 1985-10-04
; PRIOR APPLICATION NUMBER: 06/699,181
; PRIOR FILING DATE: 1985-02-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-452-817-1
Query Match 100.0%; Score 1009; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 7,6e-117;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTCVPHQPTAFCSNLDVIRAKFVGTPEVNQTTLYQREYIKWTYKGFQALGDAADIRF 60
DB 1 CTCVPHQPTAFCSNLDVIRAKFVGTPEVNQTTLYQREYIKWTYKGFQALGDAADIRF 60
OY 61 VYTPMSEVCVGFYRSHRSEFLIAGLQDGLHITTCFVAWPNSTSLAORGFRTTY 120
DB 61 VYTPMSEVCVGFYRSHRSEFLIAGLQDGLHITTCFVAWPNSTSLAORGFRTTY 120
OY 121 TVGRECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQGRHLACLIPREPGLCTWQSLR 180
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Db 121 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180
Qy 181 SQIA 184
Db 181 SQIA 184

RESULT 2
US-08-588-163-5
; Sequence 5, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,163
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-1
US-08-588-163-5

Query Match 100.0%; Score 1009; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 9e-117;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWNSLSLAORRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWNSLSLAORRGFTKTY 143
Qy 121 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180
Db 144 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 203

Qy 181 SQIA 184
Db 204 SQIA 207
RESULT 3
US-09-111-070-5
; Sequence 5, Application US/09111070
; Patent No. 5914392
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-1
US-09-111-070-5

Query Match 100.0%; Score 1009; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 9e-117;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDLVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWNSLSLAORRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWNSLSLAORRGFTKTY 143
Qy 121 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 180
Db 144 TVGCSECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPREPGLCTWQSLR 203
Qy 181 SQIA 184
Db 204 SQIA 207

RESULT 4

US-08-849-764C-5

; Sequence 5, Application US/08849764C
; Patent No. 6300310

; GENERAL INFORMATION:

; APPLICANT: GREENE, JOHN M
; ROSEN, CRAIG; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; METALLOPROTEINASE-4

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/849,764C

; FILING DATE: 19-SEP-1997

; CLASSIFICATION: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: MICHELE M. WALES

; REGISTRATION NUMBER: 43, 975

; REFERENCE/DOCKET NUMBER: PF148US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 207 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-08-849-764C-5

Query Match 100.0%; Score 1009; DB 4; Length 207;

Best Local Similarity 100.0%; Pred. No. 9e-117;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVORYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVORYEIKMTKMYKGFQALGDAADIRF 83

QY 61 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSFVAPWNSLSLAORRGFTKTY 120

Db 84 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSFVAPWNSLSLAORRGFTKTY 143

QY 121 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180

Db 144 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203

QY 181 SQIA 184

Db 204 SQIA 207

RESULT 5

US-09-262-087-5

; Sequence 5, Application US/09262087

; Patent No. 6391853

; GENERAL INFORMATION:

; APPLICANT: GREENE, JOHN M
; APPLICANT: ROSEN, CRAIG

RESULT 6

US-08-463-261B-11

; Sequence 11, Application US/08463261B

; Patent No. 6448042

; GENERAL INFORMATION:

; APPLICANT: John M. Greene and Craig A. Rosen
; CORRESPONDENCE ADDRESS: 11
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; METALLOPROTEINASE-4

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,087

; FILING DATE: 04-MAR-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/463,261

; FILING DATE: 05-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/14498

; FILING DATE: 13-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: A. ANDERS BROOKES

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF148PID1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8439

; TELEFAX: 301-309-8504

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 207 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-262-087-5

Query Match 100.0%; Score 1009; DB 4; Length 207;

Best Local Similarity 100.0%; Pred. No. 9e-117;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVORYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPHPQTAFCSNDLVIRAKFVGTPPEVNOTTLVORYEIKMTKMYKGFQALGDAADIRF 83

QY 61 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSFVAPWNSLSLAORRGFTKTY 120

Db 84 VYTPMSEVCGYFHRSHRSEEFLLAGKLDGDLHITTCSFVAPWNSLSLAORRGFTKTY 143

QY 121 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 180

Db 144 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLLQSGSEKGFQSRHLACLPRPGLCTWQSLR 203

QY 181 SQIA 184

Db 204 SQIA 207

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RESULT 8
US-08-588-163-4
; Sequence 4, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; City: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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APPLICATION NUMBER: US/08/588,163
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: METALLOPROTEINASES
CLONE: TIMP-3
US-08-588-163-4

Query Match 37.4%; Score 377.5; DB 1; Length 211;

Best Local Similarity 40.8%; Pred. No. 1.3e-38;
Matches 73; Conservative 33; Mismatches 62; Indels 11; Gaps 5;

QY 1 CTCVPHPTQATCNSDLVIRAKVGTPEVNO--TTLYORYEIKMTKTKYKGFQALGDAD 57
DB 24 CTCSSHPQDAFCNSDIVIRAKVGRKLVKEGPFGLV--YTIKQMKYRGFTKM---PH 78
QY 58 IRFVVTTPAMESVCGYFHRSHNRSEFLIAGKLQDGLLHTTCSFVAPMNSLSIAORRGFT 117
DB 79 VOYIHTSEASESLICGL--KLEVNKRYQYLLTGRVYDGMKMTGCLNFYERMDQLTISGRKGIN 136
QY 118 KTYTVGCEBCTVPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSHHACLPREPGLCTW 176
DB 137 YRHHG-C-NCKIKSCYVLPFCVFTSKNECLMTDMLSNFGYPGYQSHYACIRQKGYCSW 194

RESULT 9

US-09-111-070-4
Sequence 4, Application US/09111070
Patent No. 5914392

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

APPLICANT: Moriy, Lynn E.

TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF

TITLE OF INVENTION: METALLOPROTEINASES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/111.070

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/588.163

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0053

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 211 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: METALLOPROTEINASES

CLONE: TIMP-3

US-09-111-070-4

Query Match 37.4%; Score 377.5; DB 2; Length 211;

Best Local Similarity 40.8%; Pred. No. 1.3e-38;
Matches 73; Conservative 33; Mismatches 62; Indels 11; Gaps 5;

QY 1 CTCVPHPTQATCNSDLVIRAKVGTPEVNO--TTLYORYEIKMTKTKYKGFQALGDAD 57
DB 24 CTCSSHPQDAFCNSDIVIRAKVGRKLVKEGPFGLV--YTIKQMKYRGFTKM---PH 78
QY 58 IRFVVTTPAMESVCGYFHRSHNRSEFLIAGKLQDGLLHTTCSFVAPMNSLSIAORRGFT 117
DB 79 VOYIHTSEASESLICGL--KLEVNKRYQYLLTGRVYDGMKMTGCLNFYERMDQLTISGRKGIN 136
QY 118 KTYTVGCEBCTVPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFQSHHACLPREPGLCTW 176
DB 137 YRHHG-C-NCKIKSCYVLPFCVFTSKNECLMTDMLSNFGYPGYQSHYACIRQKGYCSW 194

RESULT 10

US-08-588-163-3
Sequence 3, Application US/08588163
Patent No. 5643752

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

APPLICANT: Moriy, Lynn E.

TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF

TITLE OF INVENTION: METALLOPROTEINASES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588.163

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0053

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 220 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: METALLOPROTEINASES

CLONE: TIMP-2

US-08-588-163-3

Query Match 37.4%; Score 377.5; DB 1; Length 220;
Best Local Similarity 41.3%; Pred. No. 1.4e-38;
Matches 76; Conservative 27; Mismatches 66; Indels 15; Gaps 6;

QY 1 CTCVPHPTQATCNSDLVIRAKVGTPEVNO--TTLYO-----RYEIKMTKTKYKGFQALG 53
DB 27 CSCSPVHQDAFCNADVIRAKAVSEKEVDGNDIYGNPIKRIQYIEIKIMFK-----G 81

Qy 54 DAADIRFVVTAPSSAVCGYFHRSHNRSEFLIAGKLO-DGLLHITTCSPVAPWNSLSLAQ 112
Db 82 PKDIEFIYTAPSSAVCG-VSLDVGKKEYLIAGKAGDGKWHITLCDFIVPWTLSSTQ 140
Qy 113 RGFTKTYTVGCECTVFPCLSPCKLQSGTHCLWTDQLLOGSEKGFQSRHLACLPRPG 172
Db 141 KASLNHRVQMGCECKITRCMPICVYISSPDECLWMDVWTEKXNNGHQAQKFFACIKRSDG 199
Qy 173 LCTW 176
Db 200 SCAW 203
RESULT 11
US-09-111-070-3
; Sequence 3, Application US/09111070
; Patent No. 5914392
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-2
US-09-111-070-3
Query Match 37.4%; Score 377.5; DB 2; Length 220;
Best Local Similarity 41.3%; Pred. No. 1.4e-38;
Matches 76; Conservative 27; Mismatches 66; Indels 15; Gaps 6;
Qy 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNO--TTLYQ-----RVEIKMTKMYKGFQALG 53
Db 27 CSCSPVHPQQAFCNADVVIRAKAVSEKVEYDSGNDIYGNPIKRIQVIEIKIMFK-----G 81
Qy 54 DAADIRFVVTAPSSAVCGYFHRSHNRSEFLIAGKLO-DGLLHITTCSPVAPWNSLSLAQ 112
Db 82 PKDIEFIYTAPSSAVCG-VSLDVGKKEYLIAGKAGDGKWHITLCDFIVPWTLSSTQ 140

Qy 113 RGFTKTYTVGCECTVFPCLSPCKLQSGTHCLWTDQLLOGSEKGFQSRHLACLPRPG 172
Db 141 KASLNHRVQMGCECKITRCMPICVYISSPDECLWMDVWTEKXNNGHQAQKFFACIKRSDG 199
Qy 173 LCTW 176
Db 200 SCAW 203
RESULT 12
US-08-849-764C-4
; Sequence 4, Application US/08849764C
; Patent No. 6300310
; GENERAL INFORMATION:
; APPLICANT: GREENE, JOHN M
; APPLICANT: ROSEN, CRAIG
; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASE-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,764C
; FILING DATE: 19-Sep-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF148US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-849-764C-4
Query Match 36.9%; Score 372; DB 4; Length 210;
Best Local Similarity 40.8%; Pred. No. 6.1e-36;
Matches 73; Conservative 31; Mismatches 63; Indels 12; Gaps 5;
Qy 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNO--TTLYQRYEIKMTKMYKGFQALGDAAD 57
Db 24 CTCSPSPHPQDAFCNCDIVIRAKVVGKLVKREGPGTLY--YTIKMKMYRGTMPHY-- 79
Qy 58 IRFVYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSPVAPWNSLSLAQRGFT 117
Db 80 --YIHTASESLCGL--KLEVNKYQYLLTGRVYDGKMYTGLCNFVERWDQLTLSQRKGLN 135
Qy 118 KTYTVGCECTVFPCLSPCKLQSGTHCLWTDQLLOGSEKGFQSRHLACLPRPGCLCTW 176
Db 136 YRYHLGC-NCKIKSCYLLPCFVTSKNECLWTDMLSNFGYQSGKHVACIRKQKGYCSW 193
RESULT 13
US-09-262-087-4
; Sequence 4, Application US/09262087

Patent No. 6391853
GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,087
FILING DATE: 04-MAR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,261
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14498
FILING DATE: 13-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF148P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-262-087-4

Query Match 36.9%; Score 372; DB 4; Length 210;
Best Local Similarity 40.8%; Pred. No. 6,1e-38;
Matches 73; Conservative 31; Mismatches 63; Indels 12; Gaps 5;

QY 1 CTCVPHPOTAFNSDLYIRAKFVGTPEVNO--TLYQRYEIKMTKMYKGFQALGDAAD 57
DB 24 CTCSPSHQDAFCNSDLYIRAKVGVKLVKEGPGITLV--YTIKQMKYRGFTTKMPHY-- 79
QY 58 IRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQDGLHITTCSFVAPWNSLSLAQRGFT 117
DB 80 --YIHTASESISLGL--KLEVNKYQYLLTGRVYDGKMTGLCNFVERWDQTLTSQRKGLN 135
QY 118 KTYVVGCECTVFPCLSTPRKLOSGTGHCLMTDQLQSGSEKGFQSHLACLPRBPLCTW 176
DB 136 YRHLGC-NCKIKSCYVLPFVTSKNELMTDMLNFGYPGYSKHVACIRQKGYCSW 193

RESULT 14
US-08-463-261B-10
Sequence 10, Application US/08463261B
Patent No. 6448042
GENERAL INFORMATION:
APPLICANT: John M. Greene and Craig A. Rosen
TITLE OF INVENTION: Human Tissue Inhibitor of Metalloproteinase-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,261B
FILING DATE: 05-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14498
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVER
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF148P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 301-610-8439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-463-261B-10

Query Match 36.9%; Score 372; DB 4; Length 210;
Best Local Similarity 40.8%; Pred. No. 6,1e-38;
Matches 73; Conservative 31; Mismatches 63; Indels 12; Gaps 5;

QY 1 CTCVPHPOTAFNSDLYIRAKFVGTPEVNO--TLYQRYEIKMTKMYKGFQALGDAAD 57
DB 24 CTCSPSHQDAFCNSDLYIRAKVGVKLVKEGPGITLV--YTIKQMKYRGFTTKMPHY-- 79
QY 58 IRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQDGLHITTCSFVAPWNSLSLAQRGFT 117
DB 80 --YIHTASESISLGL--KLEVNKYQYLLTGRVYDGKMTGLCNFVERWDQTLTSQRKGLN 135
QY 118 KTYVVGCECTVFPCLSTPRKLOSGTGHCLMTDQLQSGSEKGFQSHLACLPRBPLCTW 176
DB 136 YRHLGC-NCKIKSCYVLPFVTSKNELMTDMLNFGYPGYSKHVACIRQKGYCSW 193

RESULT 15
US-08-849-764C-3
Sequence 3, Application US/08849764C
Patent No. 6300310
GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,764C

FILING DATE: 19-Sep-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MICHELE M. WALES
REGISTRATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: PF148US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-849-764C-3

Query Match 36.6%; Score 369.5; DB 4; Length 218;
Best Local Similarity 41.0%; Pred. No. 1.3e-37;
Matches 75; Conservative 28; Mismatches 65; Indels 15; Gaps 6;

QY 1 CTCVPHPOTAFCSNDLVIRAKFVGTPEVNQ-----TTLYORYEIKMTKMYKGFQALGD 54
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
27 CSCSPVHPQQAFCNADVVIRAKVSEKVEYDGNIDYGNPIKRIYEIKI-KMEK-----GP 80
QY 55 AADIRFVYTPAMESVGYFHRSHNRSEFLIAGKLQ-DGLLHITTCSFVAPWNSLSLAOR 113
Db |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
81 EKDIEFIYTPSSAVCG-VSLDVGGKKYLIAGKAEQDGMHITLCDFIVPWDTLSTTQK 139
QY 114 RGFTTYTVGCCECTVFPCLSPCKLQSGTHCLWTDQLQSGSEKGFQSRHLACLPRPGL 173
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
140 KSLNHRVQMGCECKITRCMPICVYISSPDECLWMDWVTEKNGHQAKFFACIKRSDGS 198
QY 174 CTW 176
Db |||
199 CAW 201

Search completed: December 17, 2002, 15:06:33
Job time : 15.5931 secs

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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 18.4 Seconds
(without alignments)
961.344 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009
Sequence: 1 CTCVPPHPQTAFCNSDLVIR.....ACLPREPGLCTWGLRSQIA 184

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Sequenced: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	100.0	207	1	ZYHUEP metalloproteinase
2	1002	99.3	207	2	A34303 matrix metalloprot
3	893	88.5	207	1	A35685 metalloproteinase
4	876	86.8	207	2	I46964 metalloproteinase
5	870	86.2	207	2	I47061 collagenase inhibi
6	817.5	81.0	206	1	A33350 metalloproteinase
7	761.5	75.5	205	1	A26106 metalloproteinase
8	742	73.5	217	1	UC2557 metalloproteinase
9	382.5	37.9	220	1	UH0683 metalloproteinase
10	382.5	37.9	220	2	I53415 metalloproteinase
11	381.5	37.8	212	1	A43429 metalloproteinase
12	379.5	37.6	196	1	S38624 metalloproteinase
13	379.5	37.6	220	1	S45683 metalloproteinase
14	377.5	37.4	211	1	S45317 metalloproteinase
15	377.5	37.4	220	1	A47128 metalloproteinase
16	373.5	37.0	211	1	A53532 metalloproteinase
17	372.5	36.9	211	2	JC4630 metalloproteinase
18	370.5	36.7	220	1	A35996 metalloproteinase
19	83	8.2	4307	2	T20721 hypothetical prote
20	77.5	7.7	944	2	S66870 DN4 protein - yea
21	76.5	7.6	183	2	A32851 22K extracellular
22	75.5	7.5	433	1	B65058 fixC protein homol
23	75.5	7.5	530	2	F84488 probable Tail-like
24	75.5	7.5	1513	2	A54895 mucin 2, intestina
25	75	7.4	461	1	CGRTT1 tumor necrosis fac
26	74.5	7.4	50	2	I53729 metalloproteinase
27	74.5	7.4	430	2	S73269 histidine-tRNA lig
28	74.5	7.4	444	2	S48966 suppressor protein
29	74	7.3	158	2	F89123 protein K07C11.5 [

30	73.5	7.3	993	1	PIVXTA RNA 1 protein - to
31	73	7.2	537	2	I49135 prolyl 4-hydroxyla
32	73	7.2	555	2	D71444 probable thioester
33	72.5	7.2	611	2	A83976 hypothetical prote
34	71.5	7.1	533	2	T26860 hypothetical prote
35	71.5	7.1	581	2	T06825 ketol-acid reducto
36	71.5	7.1	1227	2	T23004 hypothetical prote
37	71.5	7.1	1339	2	JC4387 epidermal growth f
38	71	7.0	480	2	F82796 hypothetical prote
39	71	7.0	702	2	T16832 hypothetical prote
40	71	7.0	726	2	H96889 hypothetical prote
41	70.5	7.0	333	2	AF1582 molybdenum cofacto
42	70	6.9	266	2	S02510 nlfm protein - Kle
43	70	6.9	345	1	NBMS apolipoprotein H p
44	70	6.9	747	1	gene 45 protein -
45	69.5	6.9	201	2	A47220 dermatopontin prec

ALIGNMENTS

RESULT 1
ZYHUEP
Metalloproteinase tissue inhibitor 1 precursor [validated] - human
N.Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor
C.Species: Homo sapiens (man)
C.Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000
C.Accession: A93372; A93363; A23534; A20595; A35826; A48417; S20318; S15872; I52912; S664
R.Docherty, A.V.P.; Lyons, A.; Smith, B.O.; Wright, E.M.; Stephens, P.E.; Harris, T.O.R.;
Nature 318, 66-69, 1985
A>Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to ery
A.Reference number: A93372; MUID:66040463; PMID:33903517
A.Accession: A93372
A.Molecule type: mRNA
A.Residues: 1-207 <DOC>
A.Cross-references: GB:X03124; NID:937182; PIDN:CAA26902.1; PID:937183
R.Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.;
Nature 315, 768-771, 1985
A>Title: Molecular characterization and expression of the gene encoding human erythroid-1
A.Reference number: A93363; MUID:85240567; PMID:3839290
A.Accession: A93363
A.Molecule type: mRNA
A.Residues: 1-207 <GAS>
R.Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H.G.
Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986
A>Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
A.Reference number: A23534; MUID:86205964; PMID:3010309
A.Accession: A23534
A.Molecule type: mRNA
A.Residues: 1-207 <CAR>
A.Cross-references: GB:M12670; NID:g182482; PIDN:AAA52436.1; PID:g182483
A>Note: parts of this sequence were confirmed by protein sequencing
A.Note: Carboxylate binding sites were determined
R.Stricklin, G.P.; Welgus, H.G.
J. Biol. Chem. 258, 12252-12258, 1983
A>Title: Human skin fibroblast collagenase inhibitor.
A.Reference number: A20595; MUID:84032401; PMID:6313647
A.Accession: A20595
A.Molecule type: protein
A.Residues: 24-44, 'L', 46 <STR>
A>Note: six disulfide bonds are present
R.Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.I
DNA Cell Biol. 9, 479-485, 1990
A>Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.
A.Reference number: A35826; MUID:91035550; PMID:2171551
A.Accession: A35826
A.Molecule type: mRNA
A.Residues: 1-207 <RAP>
A.Cross-references: GB:M8188
R.Van Ransst, M.; Norga, K.; Maasure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van I
Cytokine 3, 231-239, 1991
A>Title: The cytokine-protease connection: identification of a 96-kD RHP-1 gelatinase and
A.Reference number: A48417; MUID:91355647; PMID:1653055

A:Accession: A48417
A:Molecule type: protein
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-52 <VAN>
A:Experimental source: monocytic cell line THP-1
A:Note: sequence modified after extraction from NCBI backbone
R:Osthues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.
FEBS Lett. 296, 16-20, 1992
A:Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)
A:Reference number: S20318; MUID:92111776; PMID:1730286
A:Accession: S20318
A:Molecule type: protein
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-38 <OST>
A:Experimental source: rheumatoid synovial fluid
R:Opdenakker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.
FEBS Lett. 284, 73-78, 1991
A:Title: Natural human monocyte gelatinase and its inhibitor.
A:Reference number: S15872; MUID:91285112; PMID:1647974
A:Accession: S15872
A:Molecule type: protein
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-42, 'X', 44, 'X', 46, 'X', 48-51 <FEB>
A:Experimental source: peripheral blood monocytes
R:Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;
Biochem. J. 268, 267-274, 1990
A:Title: Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIMP)
A:Reference number: A38978; MUID:90303199; PMID:2163605
A:Contents: annotation; disulfide bonds
R:Opbroek, A.; Kenney, M.C.; Brown, D.
Curr. Eye Res. 12, 877-883, 1993
A:Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).
A:Reference number: I52912; MUID:94123576; PMID:7507419
A:Accession: I52912
A:Status: translated from GB/EMBL/DBJ.
A:Molecule type: mRNA
A:Residues: 1-207 <RES>
A:Cross-references: GB:S68252; NID:9545022; PIDN:AAD14009.1; PID:g4261709
R:Triebel, S.; Blaaser, J.; Gote, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Tschesche, H.
Eur. J. Biochem. 231, 714-719, 1995
A:Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol
A:Reference number: S66461; MUID:953377303; PMID:7649172
A:Accession: S66461
A:Molecule type: protein
A:Residues: 24-38 <TRI>
A:Experimental source: polymorphonuclear leukocytes
C:Comment: This protein, found in a variety of body fluids, complexes with metalloprotei
s-specific, stimulating the growth and differentiation of only human and murine erythro
C:Comment: The remarkable heat stability of this protein may be due to disulfide bond fo
C:Genetics:
A:Gene: GDB:TIMP1; CLGI; TIMP
A:Cross-references: GDB:I19615; OMIM:305370
A:Map position: Xp11.3-Xp11.23
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; glycoprotein; metalloproteinase inhibitor; mitogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F:24-93,26-122,36-147,150-197,155-160,168-189/Disulfide bonds: #status experimental
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 100.0%; Score 1009; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.7e-94;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCBECTVFPCLSIPTCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSILR 180
Db 144 TVGCBECTVFPCLSIPTCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSILR 203

Qy 181 SQIA 184
Db 204 SQIA 207

RESULT 2
Jc4303
matrix metalloproteinase-1 tissue inhibitor - baboon
C:Species: Papio sp. (baboon)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 16-Jul-1999
C:Accession: Jc4303
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.
Gene 163, 267-271, 1995
A:Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of
A:Reference number: Jc4303; MUID:96011646; PMID:7590279
A:Accession: Jc4303
A:Molecule type: mRNA
A:Residues: 1-207 <FOR>
A:Cross-references: GB:L37295; NID:g561545; PIDN:AAA99943.1; PID:g561546
A:Experimental source: smooth muscle cell
C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase f
se and influences the proteinase activity. It has a role as a physiological molecule fo
C:Genetics:
A:Gene: timp-1
C:Superfamily: metalloproteinase inhibitor
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 99.3%; Score 1002; DB 2; Length 207;
Best Local Similarity 98.9%; Pred. No. 2.4e-93;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDVIRAKFVGTPPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 120
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWNSLSLAQRGFTKTY 143
Qy 121 TVGCBECTVFPCLSIPTCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSILR 180
Db 144 TVGCBECTVFPCLSIPTCKLQSGTHCLWTDQLQSGEKGFQSRHLACLPREPGLCTWQSILR 203

Qy 181 SQIA 184
Db 204 TRIA 207

RESULT 3
A35685
metalloproteinase inhibitor 1 precursor - bovine
N:Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhibi
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C:Accession: A35685; B34468; B29712; A34833; I46979
R:Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 171, 250-256, 1990
A:Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression
A:Reference number: A35685; MUID:90365711; PMID:2393392
A:Accession: A35685
A:Molecule type: mRNA
A:Residues: 1-207 <FRE>
A:Cross-references: GB:M60073; NID:g163760; PIDN:AAA30784.1; PID:g163761
R:De Clerck, Y.A.; Yeon, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.
J. Biol. Chem. 264, 17445-17453, 1989
A:Title: Purification and characterization of two related but distinct metalloproteinase
A:Reference number: A34468; MUID:90008914; PMID:2551903
A:Accession: B34468
A:Molecule type: protein
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>

A:Experimental source: culture medium of aortic endothelial cells
R:Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Streeck, B./Technology 5, 595-598, 1987
A:Title: Molecular cloning and synthesis of biologically active human tissue inhibitor C
A:Reference number: A29712
A:Accession: B29712
A:Molecule type: protein
A:Residues: 24-37 <KAC>
A:Experimental source: culture medium of fibroblastic BC 21 cells
R:Moses, M.A.; Sudhalter, J.; Langer, R.
Science 248, 1408-1410, 1990
A:Title: Identification of an inhibitor of neovascularization from cartilage.
A:Reference number: A34833; MUID:90288433; PMID:1694043
A:Accession: A34833
A:Molecule type: protein
A:Residues: 24-51 <MOS>
A:Experimental source: cartilage
R:Ch, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.
Reprod. 50, 835-844, 1994
A:Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct
A:Reference number: 146979; MUID:94257757; PMID:8199264
A:Accession: 146979
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <SAT>
A:Cross-references: GB:S70841; NID:g546973; PIDN:AA830892.1; PID:g546974
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases
A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns
C:Keywords: metalloproteinase inhibitor
C:Keywords: erythropoiesis, extracellular matrix, glycoprotein; metalloproteinase inhibitor
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F:24-93,26-122,36-147,150-157,155-160,168-189/Disulfide bonds: #status predicted
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.5%; Score 893; DB 1; Length 207;
Best Local Similarity 87.0%; Pred. No. 2,3e-82;
Matches 160; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Q 1 CTCVPHQPTAFCSNDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGPAADIRF 60
Db 24 CTCVPHQPTAFCSNDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGPAADIRF 83

Q 61 VYTPAMSVCGYFHRSHNRSEFLIAGKLDGLHITTCSPVAPWNSLSLAQRGFTKTY 120
Db 84 IYTPAMSVCGYFHRSHNRSEFLIAGKLDGLHITTCSPVAPWNSLSLAQRGFTKTY 143

Q 121 TVGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGSRHLACLPRPGLCTWOSLR 180
Db 144 AAGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGSRHLACLPRPGLCTWOSLR 203

Qy 181 SQIA 184
Db 204 AQMA 207

RESULT 4
146964
metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 19-Jan-2001
C:Accession: 146964
R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.
Endocrinology 134, 344-352, 1994
A:Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: c
eal tissue.
A:Reference number: 146964; MUID:94102210; PMID:8275949
A:Accession: 146964
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-207 <SMI>
A:Cross-references: GB:567450; NID:g456989; PIDN:AA829472.1; PID:g456990
C:Superfamily: metalloproteinase inhibitor

Query Match 86.8%; Score 876; DB 2; Length 207;
Best Local Similarity 86.7%; Pred. No. 1,2e-80;
Matches 156; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Q 1 CTCVPHQPTAFCSNDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGPAADIRF 60
Db 24 CTCVPHQPTAFCSNDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGPAADIRF 83

Q 61 VYTPAMSVCGYFHRSHNRSEFLIAGKLDGLHITTCSPVAPWNSLSLAQRGFTKTY 120
Db 84 IYTPAMSVCGYFHRSHNRSEFLIAGKLDGLHITTCSPVAPWNSLSLAQRGFTKTY 143

Q 121 TVGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGSRHLACLPRPGLCTWOSLR 180
Db 144 AAGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGSRHLACLPRPGLCTWOSLR 203

Qy 181 SQIA 184
Db 204 PRVA 207

RESULT 5
147061
collagenase inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C:Accession: 147061
R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.
Mol. Cell. Endocrinol. 83, 65-71, 1992
A:Title: Differential screening of ovarian cDNA libraries detected the expression of the
A:Reference number: 147061; MUID:92201478; PMID:1312961
A:Accession: 147061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TMN>
A:Cross-references: GB:596211; NID:g247729; PIDN:AA821865.1; PID:g247730
C:Superfamily: metalloproteinase inhibitor

Query Match 86.2%; Score 870; DB 2; Length 207;
Best Local Similarity 83.7%; Pred. No. 4,7e-80;
Matches 154; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Q 1 CTCVPHQPTAFCSNDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGPAADIRF 60
Db 24 CTCVPHQPTAFCSNDLVIRAKFVGTPEVNOTTLVYRVEIKMTKMYKGFQALGPAADIRF 83

Q 61 VYTPAMSVCGYFHRSHNRSEFLIAGKLDGLHITTCSPVAPWNSLSLAQRGFTKTY 120
Db 84 IYTPAMSVCGYFHRSHNRSEFLIAGKLDGLHITTCSPVAPWNSLSLAQRGFTKTY 143

Q 121 TVGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGSRHLACLPRPGLCTWOSLR 180
Db 144 AAGCECTVPFCLSPCKLQSGTHCLMTDQLLQSGEKFGSRHLACLPRPGLCTWOSLR 203

Qy 181 SQIA 184
Db 204 PRVA 207

RESULT 6
A33350
metalloproteinase inhibitor 1 precursor - rabbit
N:Alternate names: TIMP-1; tissue inhibitor of metalloproteinases 1
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Jun-1992 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C:Accession: A33350; A30864
R:Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Nocter, R.H.; Quible, D.J.
J. Biol. Chem. 267, 7092-7095, 1992
A:Title: Hypertoxic exposure alters gene expression in the lung. Induction of the tissue i
A:Reference number: A33350; MUID:89214135; PMID:2708356
A:Accession: A33350
A:Molecule type: mRNA

A;Residues: 168-193,'L','195-205 <SKU>
A;Cross-references: GB:I00755; GB:J00425; NID:g5l554; PIDN:CAA24132.1; PID:g817965
A;Note: authors thought this clone represented a form of interferon beta
C;Genetics:
A;Gene: Timp
A;Map position: X
A;Introns: 41/3; 68/3; 110/3; 152/3
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agents
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns
C;Superfamily: metalloproteinase inhibitor
F;Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-205/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
F;25-94, 27-123, 37-148, 151-197, 156-161, 169-189/disulfide bonds: #status predicted
F;54,102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.5%; Score 761.5; DB 1; Length 205;
Best Local Similarity 73.7%; Pred.No. 3.9e-69;
Matches 132; Conservative 25; Mismatches 21; Indels 1; Gaps 1;

QY 1 CTCVPHPTQAFNCSDLIVIRAKFTGTVGVNQTTLYQRVEIKMTVMYKGFQALGDADIRF 60
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 25 CSCAPHPQTAFNCSDLIVIRAKFTWSPSEINETTLYQRYKI KMTVKMLGFKAVGNAADIRY 84
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 VYTPAMESVCGYHRSHNRSEEFILACKLDGLLIHTTCSVPAPWNSISLAORSGFTKTY 120
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 AYTPTMESLCGYAHKSQNRSSEEFITLRNLGNLUHSACSLPLVWPRTLSPPAQRAFSTKY 144
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TVGCECTVPFCISIPCKLOSGTHCLMTDQLLOGSERKFQSRLHACLPRPEGLCTWQSL 179
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 145 SAGCGCVTFPCISIPCKLESDDHCLMTDQVLVGSE-DYQSRHFACLP RNPGLCTWRSL 202
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
JC2557
Metalloproteinase inhibitor 1 precursor - rat
N;Alternate names: TIMP-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence,revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC2557; B39120; S20326
R;Okada, A.; Garnier, J.M.; Vicaire, S.; Bassett, P.
Gene 147, 301-302, 1994
A;Title: Cloning of the cDNA encoding rat tissue inhibitor of metalloproteinase 1 (TIMP-1)
A;Reference number: JC2557; MUID:95011636; PMID:7926820
A;Accession: JC2557
A>Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <OKA>
A;Cross-references: EMBL:U06179; NID:g468057; PIDN:AAA85780.1; PID:g468058
R;Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Razza, M.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991
A;Title: Angiotensin II induces secretion of plasminogen activator inhibitor 1 and a tissue inhibitor of metalloproteinase 1 from endothelial cells
A;Reference number: A39120; MUID:91156719; PMID:2000398
A;Accession: B39120
A>Status: preliminary
A;Molecule type: protein
A;Residues: 24-36,'B','38','B',40-42,'X',44 <OLS>
R;Roswit, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, J.J.
Arch. Biochem. Biophys. 292, 402-410, 1992
A;Title: Purification and sequence analysis of two rat tissue inhibitors of metalloproteinase
A;Reference number: S20325; MUID:92117648; PMID:1309971
A;Accession: S20326
A;Molecule type: protein
A;Residues: 24-45 <ROS>
C;Function:
A;Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
A;Note: controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating activity
A;Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agents
A;Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns
C;Superfamily: metalloproteinase inhibitor

C,Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibitor
 F:1-23/Domains: signal sequence #status predicted <SIG>
 F:24-217/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
 F:101,130/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 73.5%; Score 742; DB 1; Length 217;
 Best Local Similarity 71.5%; Pred. No. 3,8e-67;
 Matches 128; Conservative 23; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCVPHPOTAFCSNDLVIRAKFVGTPPEVNO-TTLVYQ-----RYEIKMTKMYKGFQALG 60
 DB 24 CSCAPTHPOTAFCSNDLVIRAKFMGSPETLETLVYQRYEIKMTKMYKGFDAVGNATGFRF 83
 QY 61 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLQDGLHTTCSFPVAPMNSLSLAQRGFTKY 120
 DB 84 AYTAMESICGVVHKSQNRSEEFLLIAGRNRNMLHTTACSFVPMHNSLPAAQKAFVKTY 143
 QY 121 TVGCECTVFPCLSIPTCKLQSGTHCLMTDQLQSGSEKGFQSHHLACLPREPGLCTWOST 179
 DB 144 SAGCGVCTVFPCLSIPTCKLQSGTHCLMTDQLQSGSEKGYQSDHFACTPRNPDLCTWQYL 202

RESULT 9

QY 1 metalloproteinase inhibitor 2 precursor - mouse
 N,Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
 C,Species: Mus musculus (house mouse)
 C,Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999

C,Accession: J00683; J01234; S18428; S15987; S26189
 R,Shimizu, S.; Malik, K.; Sejima, H.; Kishi, J.; Hayakawa, T.; Koiwai, O.
 A,Title: Cloning and sequencing of the cDNA encoding a mouse tissue inhibitor of metalloproteinase
 A,Reference number: J00683; MUID:92290292; PMID:1601312
 A,Accession: J00683

A,Molecule type: mRNA
 A,Residues: 1-220 <SH1>

A,Cross-references: EMBL:X62622; NID:G54801; PIDN:CAA4491.1; PID:G54802

A,Experimental source: 3T3 fibroblast, strain Balb/c

R,Lecco, K.J.; Hayden, L.J.; Sharma, R.R.; Rocheleau, H.; Greenberg, A.H.; Edwards, D.R.
 Gene 117, 209-217, 1992

A,Title: Differential regulation of TIMP-1 and TIMP-2 mRNA expression in normal and Ha-r

A,Reference number: J01234; MUID:92347695; PMID:1639268

A,Molecule type: mRNA
 A,Accession: J01234

A,Residues: 1-11, 'H', '13-20', 'L', '22-194', 'E', '196-220' <IEC>

A,Cross-references: GB:M93934; NID:G202053; PIDN:AAA40446.1; PID:G202054

R,Kishi, J.

M,XX 11, 373, 1991

A,Title: Correction.

A,Accession: S18428

A,Reference number: S18428; MUID:92244125; PMID:1667327

A,Molecule type: protein
 A,Residues: 27-46, 'H', '48-50-53', 'VD', '56', 'DY', <KIS>

R,Kishi, J.; Ogawa, K.; Yamamoto, S.; Hayakawa, T.
 Matrix 11, 10-16, 1991

A,Title: Purification and characterization of a new tissue inhibitor of metalloproteinase

A,Reference number: S15987; MUID:91226375; PMID:1851244

A,Molecule type: protein
 A,Residues: 27-46, 'HLX', '50-52', 'LX', '55-56', 'DDX', '60', 'X', '62' <KI2>

A,Note: this sequence has been revised in reference S18428

A,Function:

C,Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase

C,Superfamily: metalloproteinase inhibitor
 C,Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen

F:1-26/Domains: signal sequence #status predicted <SIG>
 F:1-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>

F:27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 37.9%; Score 382.5; DB 1; Length 220;
 Best Local Similarity 41.8%; Pred. No. 5.9e-31;
 Matches 77; Conservative 27; Mismatches 65; Indels 15; Gaps 6;

QY 1 CTCVPHPOTAFCSNDLVIRAKFVGTPPEVNO-TTLVYQ-----RYEIKMTKMYKGFQALG 53
 DB 27 CSCSPVHQAFCSNDLVIRAKVSEKEVDGNDLYGNPIKRIQYEIQIKMF-----G 81

QY 54 DADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLQ-DGLHTTCSFPVAPMNSLSLAQ 112
 DB 82 PDKDIEFIYTPASSAVCG-VSLDVCGKKEVLIAGKAEGDKMHTLCPFIWPDITLSITQ 140

QY 113 RRGFTKTYTGCECTVFPCLSIPTCKLQSGTHCLMTDQLQSGSEKGFQSHHLACLPREPGLCTWOST 172
 DB 141 KKSLSNRHYQMG-CCKITRCPMIPCYISSPDECLMMDWTEKSLNGHQAQKFACTKRSQG 199

QY 173 LCTW 176
 DB 200 SCAM 203

RESULT 10

QY 1 metalloproteinase inhibitor of metalloproteinase type 2 - rat
 C,Species: Rattus sp. (rat)
 C,Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 16-Jul-1999

C,Accession: I53415
 R,Santoro, M.; Battaglia, C.; Zhang, L.; Carlomagno, F.; Martelli, M.L.; Salvatore, D.; I
 Exp. Cell Res. 213, 398-403, 1994
 A,Title: Cloning of the rat tissue inhibitor of metalloproteinases type 2 (TIMP-2) gene:
 A,Reference number: I53415; MUID:94328839; PMID:8050496

A,Accession: I53415

A,Status: preliminary; translated from GB/EMBL/DBJ

A,Molecule type: mRNA

A,Residues: 1-220 <RES>

A,Cross-references: GB:S72594; NID:G619232; PIDN:AAC60687.1; PID:G619233

C,Genetics:

A,Superfamily: metalloproteinase inhibitor

Query Match 37.9%; Score 382.5; DB 2; Length 220;
 Best Local Similarity 41.8%; Pred. No. 5.9e-31;
 Matches 77; Conservative 27; Mismatches 65; Indels 15; Gaps 6;

QY 1 CTCVPHPOTAFCSNDLVIRAKFVGTPPEVNO-TTLVYQ-----RYEIKMTKMYKGFQALG 53
 DB 27 CSCSPVHQAFCSNDLVIRAKVSEKEVDGNDLYGNPIKRIQYEIQIKMF-----G 81

QY 54 DADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLQ-DGLHTTCSFPVAPMNSLSLAQ 112
 DB 82 PDKDIEFIYTPASSAVCG-VSLDVCGKKEVLIAGKAEGDKMHTLCPFIWPDITLSITQ 140

QY 113 RRGFTKTYTGCECTVFPCLSIPTCKLQSGTHCLMTDQLQSGSEKGFQSHHLACLPREPGLCTWOST 172
 DB 141 KKSLSNRHYQMG-CCKITRCPMIPCYISSPDECLMMDWTEKSLNGHQAQKFACTKRSQG 199

QY 173 LCTW 176
 DB 200 SCAM 203

RESULT 11

QY 1 metalloproteinase inhibitor 3 precursor - chicken
 N,Alternate names: 21K extracellular matrix protein; TIMP-3; tissue inhibitor of metalloproteinase
 C,Species: Gallus gallus (chicken)
 C,Date: 04-Mar-1993 #sequence revision 12-Apr-1996 #text_change 18-Jun-1999

C,Accession: A43429; A39043

R,Pavloff, N.; Staskus, P.W.; Kishnani, N.S.; Hawkes, S.P.
 J. Biol. Chem. 267, 17321-17326, 1992

A,Title: A new inhibitor of metalloproteinases from chicken: ChIMP-3. A third member of t

A,Reference number: A43429; MUID:92381050; PMID:1512267

A,Accession: A43429

A,Molecule type: mRNA

A,Residues: 1-212 <PAV>

A,Cross-references: GB:M94531; NID:G211901; PIDN:AAA48813.1; PID:G211902

A:Experimental source: ten-day old embryo cdna library
A:Note: sequence extracted from NCBI backbone (NCBIN:111960, NCBI:P:111961)
R:Staskus, P.W.; Mastarz, F.R.; Pallanck, L.J.; Hawkes, S.P.
J. Biol. Chem. 266, 449-454, 1991
A:Title: The 21-kDa protein is a transformation-sensitive metalloproteinase inhibitor of
A:Reference number: A39043; MUID:91093162; PMID:1845973
A:Accession: A39043
A:Molecule type: protein
A:Residues: 26-51, 1-53 <STA>
A:Experimental source: cultured embryonic fibroblasts infected with Rous sarcoma virus
A:Note: contains disulfide bonds; not glycosylated; has inhibitory activity
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agents
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns
C:Superfamily: metalloproteinase inhibitor
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-212/Product: metalloproteinase inhibitor 3 #status experimental <MAT>
F:25-92,27-119,37-144,146-193,151-156,164-185/Disulfide bonds: #status predicted
F:208/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match 37.8%; Score 381.5; DB 1; Length 212;
Best Local Similarity 40.1%; Pred. No. 7.2e-31; Mismatches 67; Indels 7; Gaps 4;
Matches 71; Conservative 32

Qy 1 CTCVPPHPQTAFCSNLDLIRAKFVGTPEVNO-TTL-YQRYEIKWTMYKGFQALGDAADIR 59
Db 25 CTCVPIHPDACSNDLIRAKVGVCKLMDKGGPFGTMRVTYVKMKMGVGFQIM---PHVQ 81
Qy 60 FVYTPAMESVCGYFHRSHNRSEFLIAGLQDGLLHITTCFSFVAPWNSLSLAQRGFTKT 119
Db 82 YIYTEASESLCGV--KLEVNKYQYLITGRVYEGKVYGLCNWYKWDRLTSLQKGLNHR 139
Qy 120 YTVGCECTVFPCLSTPCKLQSGTHCLWTDLQLOGSEKGFQSRHLACLPRPGLCTW 176
Db 140 YHLGC-GCKIRPCYILPCPATSKNECIWMLSNFGHSGHQAHYACIQRVGYCSW 195

RESULT 12
S38624
N:Alternate names: TIMP-2 precursor - long-tailed hamster (fragment)
C:Species: Crictetus longicaudatus (long-tailed hamster)
C:Date: 06-Jan-1995 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
A:Accession: S38624
R:Suzuki, Y.
Submitted to the EMBL Data Library, November 1993
A:Reference number: S38624
A:Accession: S38624
A:Molecule type: mRNA
A:Residues: 1-196 <SU2>
A:Cross-references: EMBL:X75924; NID:G414876; PIDN:CAA53528.1; PID:G414877
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
A:Note: controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F:3-196/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F:3-74,5-103,15-128,130-177,135-140,148-169/Disulfide bonds: #status predicted

Query Match 37.6%; Score 379.5; DB 1; Length 196;
Best Local Similarity 41.8%; Pred. No. 1e-30;
Matches 77; Conservative 26; Mismatches 66; Indels 15; Gaps 6;

Qy 1 CTCVPPHPQTAFCSNLDLIRAKFVGTPEVNO-TTLQY-----RYEIKWTMYKGFQALG 53
Db 3 CSCSPVHPQQAFCNADVVIRAKVSEKVDGNDIYGNPIKRIQVEIKRMFK-----G 57
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGLQ-DGLLHITTCFSFVAPWNSLSLAQ 112
Db 58 PKDTEFIYTPASSAVCG-VSLDVGGKKEYLIAGKAEKGGKWHITLCDFIVPWDTLSTTQ 116

Qy 113 RRGFTKTYTVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLOGSEKGFQSRHLACLPRPBG 172
Db 117 KKSLSNHRVQMGCG-ECKITRCMPICYISSPDECLMMDWVTEKSIINGHQAKFACIKRSDG 175
Qy 173 LCTW 176
Db 176 SCAM 179

RESULT 13
S45683
N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S45683; S20325; S60160
R:Cook, T.F.; Burke, J.S.; Bergman, K.D.; Quinn, C.O.; Jeffrey, J.J.; Partridge, N.C.
Arch. Biochem. Biophys. 311, 313-320, 1994
A:Title: Cloning and regulation of rat tissue inhibitor of metalloproteinases-
A:Reference number: S45683; MUID:94263207; PMID:8203893
A:Accession: S45683
A:Molecule type: mRNA
A:Residues: 1-220 <COO>
A:Cross-references: GB:U14526; NID:G540204; PIDN:AAA21553.1; PID:G540205
R:Roswit, W.T.; McCourt, D.W.; Partridge, N.C.; Jeffrey, J.J.
Arch. Biochem. Biophys. 292, 402-410, 1992
A:Title: Purification and sequence analysis of two rat tissue inhibitors of metallopro-
A:Reference number: S20325; MUID:92117648; PMID:1309971
A:Accession: S20325
A:Molecule type: protein
A:Residues: 27-48 <ROS>
R:Gibbons, K.L.; O'Grady, R.L.; Piper, A.A.
Submitted to the EMBL Data Library, June 1995
A:Description: Rat tissue inhibitor of metalloproteinases-2: cDNA cloning and sequence
A:Reference number: S60160
A:Accession: S60160
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-6, 'S', 8-20, 'V', 22-152, 'E', 154-220 <GIB>
A:Cross-references: EMBL:L31884
C:Genetics:
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
A:Note: controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F:1-26/Domain: signal sequence #status predicted <SIG>
F:1-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F:27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

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Best Local Similarity 41.3%; Pred. No. 1.2e-30;
Matches 76; Conservative 28; Mismatches 65; Indels 15; Gaps 6;

Qy 1 CTCVPPHPQTAFCSNLDLIRAKFVGTPEVNO-TTLQY-----RYEIKWTMYKGFQALG 53
Db 27 CSCSPVHPQQAFCNADVVIRAKVSEKVDGNDIYGNPIKRIQVEIKRMFK-----G 81
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGLQ-DGLLHITTCFSFVAPWNSLSLAQ 112
Db 82 PKDTEFIYTPASSAVCG-VSLDVGGKKEYLIAGKAEKGGKWHITLCDFIVPWDTLSTTQ 140
Qy 113 RRGFTKTYTVGCECTVFPCLSIIPCKLQSGTHCLWTDLQLOGSEKGFQSRHLACLPRPBG 172
Db 141 KKSLSNHRVQMGCG-QCKITRCMPICYISSPDECLMMDWVTEKSIINGHQAKFACIKRSDG 199
Qy 173 LCTW 176
Db 200 SCAM 203

RESULT 14

545317
metalloproteinase inhibitor 3 precursor [validated] - human
N/Alternate names: m19-5 protein; TIMP-3; tissue inhibitor of metalloproteinases 3
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence revision 12-Apr-1996 #text change 08-Dec-2000
C/Accession: S45317; S59515; S53870; I38023; A49614; C56937; I53025; S47041
R/Uris, J.A.; Ferrando, A.A.; Velasco, G.; Freije, J.M.P.; Lopez-Otin, C.
Cancer Res. 54, 2091-2094, 1994
A>Title: Structure and expression in breast tumors of human TIMP-3, a new member of the
A/Reference number: S45317; MUID:94228524; PMID:8174111
A/Accession: S45317
A/Molecule type: mRNA
A/Residues: 1-211 <URI>
A/Cross-references: EMBL:X76227; NID:G495251; PIDD:CAA53813.1; PID:G495252
A/Experimental source: breast tumor cDNA library
R/Silbiger, S.M.; Jacobsen, V.L.; Cupples, R.L.; Koski, R.A.
Gene 141, 293-297, 1994
A>Title: Cloning of cDNAs encoding human TIMP-3, a novel member of the tissue inhibitor
A/Reference number: S59515; MUID:94215920; PMID:8163205
A/Accession: S59515
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-211 <SLIP>
A/Cross-references: EMBL:U02571; NID:G472309; PIDD:AA17672.1; PID:G472310
R/Kishanani, N.S.; Staakus, P.W.; Yang, T.T.; Mastarz, F.R.; Hawkes, S.P.
Matrix Biol. 11, 479-488, 1994
A>Title: Identification and characterization of human tissue inhibitor of metalloproteinase
A/Reference number: S53870
A/Accession: S53870
A/Molecule type: protein
A/Residues: 'X',25,'XX',28,'X',30-35,'X',37,'X',39-41 <KIS>
R/Wick, M.; Burger, C.; Brunselbach, S.; Lucibello, F.C.; Mueller, R.
J. Biol. Chem. 269, 18953-18960, 1994
A>Title: A novel member of human tissue inhibitor of metalloproteinases (TIMP) gene family
A/Reference number: I38023; MUID:94308155; PMID:8034652
A/Accession: I38023
A/Molecule type: mRNA
A/Residues: 1-15,'W',17,'T',20-21,'PR',24-201,'X',203-211 <RES>
A/Cross-references: EMBL:Z30183; NID:G520931; PIDD:CAA62918.1; PID:G520932
A/Experimental source: fibroblast cell line WI-38
R/Apte, S.S.; Matei, M.G.; Olsen, B.R.
Genomics 19, 86-90, 1994
A>Title: Cloning of the cDNA encoding human tissue inhibitor of metalloproteinase-3 (TIMP-3)
A/Reference number: A49614; MUID:94245184; PMID:8188246
A/Accession: A49614
A/Molecule type: mRNA
A/Residues: 14-20,'R',23-211 <APT>
A/Cross-references: GB:U5078; NID:G407034; PIDD:AAA21815.1; PID:G407035
A/Experimental source: placenta cDNA library
R/Apte, S.S.; Olsen, B.R.; Murphy, G.
J. Biol. Chem. 270, 14313-14318, 1995
A>Title: The gene structure of tissue inhibitor of metalloproteinases (TIMP)-3 and its
A/Reference number: A56937; MUID:95301511; PMID:7782289
A/Accession: C56937
A/Molecule type: protein
A/Residues: 'X',25,'X',27-35,'X',37 <AP2>
R/Wild, C.G.; Hawlin, P.R.; Coleman, R.T.; Levine, W.B.; Deleage, A.M.; Okamoto, P.N.
DNA Cell Biol. 13, 711-718, 1994
A>Title: Cloning and characterization of human tissue inhibitor of metalloproteinase-3
A/Reference number: I53025; MUID:95290091; PMID:7772252
A/Accession: I53025
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-211 <R23>
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A/Gene: GDB:TIMP3
A/Cross-references: GDB:138175; OMIM:188826
A/Map position: 22q12.1-22q13.2
C/Function:
A/Note: Transcription induced by cytokines, tumor promoters, and anti-inflammatory agents.
A/Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression pattern.

C:Superfamily: metalloprotease inhibitor
C:Keywords: extracellular matrix; metalloprotease inhibitor
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F:24-211/Product: metalloprotease inhibitor 3 #status experimental <MAT>
F:24-91,26-118,36-143,145-192,150-155,163-184/Distalide bonds: #status predicted

Query Match 37.4% Score 377.5; DB 1; Length 211;
Best Local Similarity 40.8%; Pred. No. 1,8e-30;
Matches 73; Conservative 33; Mismatches 62; Indels 11; Gaps 5;

QY 1 CTCVPHPTACNSNDLVRKAFVGTPEVNO--TTLQRYEIKMTKMYGQALGDAAD 57
Db 24 CTCSPSHQDARCNNDIVIRAKVGVKKLVKEGPGTLV--YTIKQMKMYGFTGM--PH 78
QY 58 IREVTTPAMESVCGYFHRSNRSSEFLNGLKODGLLHTTCSFPAWNSLSLAQRGFT 117
Db 79 VQYIHTAESSESLCGL--KLEVNKKQYLLTGRVYDGKMYTGLCNFVERMDTLTSQRKGLN 136
QY 118 KTYTVGCEGCTVFPCLSLIPCKLQSGTHCLMTDQLGSEKGFPSRHLACLPREGLCITW 176
Db 137 YRYHGLQC-NCKTKSCYLLCFVTSKNECLMTDMLSNFGPYGYSKHYACIRQKGYCSW 194

RESULT 15
A37128
metallopeptinase inhibitor 2 precursor [validated] - human
N:Alternate names: chondrocyte-derived angiogenesis inhibitor; TIMP-2; tissue inhibitor of metalloproteinase
C:Species: Homo sapiens (man)
C:Date: 08-Mar-1991 #sequence revision 12-Apr-1996 #ext change 08-Dec-2000
C:Date: A37128; B35996; A34464; A34415; S21303; S20319; S17165; S58794
C:Section: Stevenson, W.G.; Brown, P.D.; Ontsoto, M.; Levy, A.T.; Liotta, L.A.
J: Biol. Chem. 265, 13933-13938, 1990
A:Title: Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in tumor cell
A:Reference number: A37128; MUID:90338014; PMID:2380196
A:Accession: A37128
A:Molecule type: mRNA
A:Residues: 1-220 <STE>
A:Cross-references: GB:J05593; NID:g339706; PIDN:AAA61186.1; PID:g339707
A:Experimental source: A2058 melanoma cell cDNA library
J: Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990
A:Title: cDNA cloning and expression of a metalloproteinase inhibitor related to tissue inhibitor of metalloproteinase
A:Reference number: A35996; MUID:90207285; PMID:215714
A:Accession: B35996
A:Molecule type: mRNA
A:Residues: 1-220 <BOO>
A:Cross-references: GB:M2304; NID:g187522; PIDN:AAA59581.1; PID:g307195
A:Experimental source: fetal aorta cDNA library
J: Stetler-Stevenson, W.G.; Kruttsch, H.C.; Liotta, L.A.
J: Biol. Chem. 264, 1374-1378, 1989
A:Title: Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metalloprotease inhibitor family
A:Reference number: A34464; MUID:9008902; PMID:2793861
A:Accession: A34464
A:Molecule type: protein
A:Residues: 27-77,'K','79-81','I','83-100','E','102-117,119-121','R','123-149','Q','151-174','T','175-188','S','190-192','G','194-196','D','198-200','E','202-204','K','206-208','G','210-212','S','214-216','D','218-220','E','222-224','K','226-228','G','230-232','S','234-236','D','238-240','E','242-244','K','246-248','G','250-252','S','254-256','D','258-260','E','262-264','K','266-268','G','270-272','S','274-276','D','278-280','E','282-284','K','286-288','G','290-292','S','294-296','D','298-300','E','302-304','K','306-308','G','310-312','S','314-316','D','318-320','E','322-324','K','326-328','G','330-332','S','334-336','D','338-340','E','342-344','K','346-348','G','350-352','S','354-356','D','358-360','E','362-364','K','366-368','G','370-372','S','374-376','D','378-380','E','382-384','K','386-388','G','390-392','S','394-396','D','398-400','E','402-404','K','406-408','G','410-412','S','414-416','D','418-420','E','422-424','K','426-428','G','430-432','S','434-436','D','438-440','E','442-444','K','446-448','G','450-452','S','454-456','D','458-460','E','462-464','K','466-468','G','470-472','S','474-476','D','478-480','E','482-484','K','486-488','G','490-492','S','494-496','D','498-500','E','502-504','K','506-508','G','510-512','S','514-516','D','518-520','E','522-524','K','526-528','G','530-532','S','534-536','D','538-540','E','542-544','K','546-548','G','550-552','S','554-556','D','558-560','E','562-564','K','566-568','G','570-572','S','574-576','D','578-580','E','582-584','K','586-588','G','590-592','S','594-596','D','598-600','E','602-604','K','606-608','G','610-612','S','614-616','D','618-620','E','622-624','K','626-628','G','630-632','S','634-636','D','638-640','E','642-644','K','646-648','G','650-652','S','654-656','D','658-660','E','662-664','K','666-668','G','670-672','S','674-676','D','678-680','E','682-684','K','686-688','G','690-692','S','694-696','D','698-700','E','702-704','K','706-708','G','710-712','S','714-716','D','718-720','E','722-724','K','726-728','G','730-732','S','734-736','D','738-740','E','742-744','K','746-748','G','750-752','S','754-756','D','758-760','E','762-764','K','766-768','G','770-772','S','774-776','D','778-780','E','782-784','K','786-788','G','790-792','S','794-796','D','798-800','E','802-804','K','806-808','G','810-812','S','814-816','D','818-820','E','822-824','K','826-828','G','830-832','S','834-836','D','838-840','E','842-844','K','846-848','G','850-852','S','854-856','D','858-860','E','862-864','K','866-868','G','870-872','S','874-876','D','878-880','E','882-884','K','886-888','G','890-892','S','894-896','D','898-900','E','902-904','K','906-908','G','910-912','S','914-916','D','918-920','E','922-924','K','926-928','G','930-932','S','934-936','D','938-940','E','942-944','K','946-948','G','950-952','S','954-956','D','958-960','E','962-964','K','966-968','G','970-972','S','974-976','D','978-980','E','982-984','K','986-988','G','990-992','S','994-996','D','998-1000','E','1002-1004','K','1006-1008','G','1010-1012','S','1014-1016','D','1018-1020','E','1022-1024','K','1026-1028','G','1030-1032','S','1034-1036','D','1038-1040','E','1042-1044','K','1046-1048','G','1050-1052','S','1054-1056','D','1058-1060','E','1062-1064','K','1066-1068','G','1070-1072','S','1074-1076','D','1078-1080','E','1082-1084','K','1086-1088','G','1090-1092','S','1094-1096','D','1098-1100','E','1102-1104','K','1106-1108','G','1110-1112','S','1114-1116','D','1118-1120','E','1122-1124','K','1126-1128','G','1130-1132','S','1134-1136','D','1138-1140','E','1142-1144','K','1146-1148','G','1150-1152','S','1154-1156','D','1158-1160','E','1162-1164','K','1166-1168','G','1170-1172','S','1174-1176','D','1178-1180','E','1182-1184','K','1186-1188','G','1190-1192','S','1194-1196','D','1198-1200','E','1202-1204','K','1206-1208','G','1210-1212','S','1214-1216','D','1218-1220','E','1222-1224','K','1226-1228','G','1230-1232','S','1234-1236','D','1238-1240','E','1242-1244','K','1246-

A:Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)
A:Reference number: S20318; MUID:92111776; PMID:1730286
A:Accession: S20319
A:Molecule type: protein
A:Residues: 'X',28,'X',30-38,'X',40-41 <OST>
A:Experimental source: rheumatoid synovial fluid
R:Ward, R.V.; Hembry, R.M.; Reynolds, J.J.; Murphy, G.
Biochem. J. 278, 179-187, 1991
A:Title: The purification of tissue inhibitor of metalloproteinases-2 from its 72 kDa protein
A:Reference number: S17165; MUID:91354200; PMID:1909113
A:Accession: S17165
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27,'X',29,'X',31-38 <WAR>
R:Ohba, Y.; Goto, Y.; Kimura, Y.; Suzuki, F.; Hisa, T.; Takahashi, K.; Takigawa, M.
Biochim. Biophys. Acta 1245, 1-8, 1995
A:Title: Purification of an angiogenesis inhibitor from culture medium conditioned by a
A:Reference number: S58794; MUID:95383380; PMID:7544625
A:Accession: S58794
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-37 <OHB>
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A:Gene: GDB:TIMP2
A:Cross-references: GDB:132612; OMIM:188825
A:Map position: 17q25-17q25
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>
F:27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 37.4%; Score 377.5; DB 1; Length 220;
Best Local Similarity 41.3%; Pred. No. 1.9e-30;
Matches 76; Conservative 27; Mismatches 66; Indels 15; Gaps 6;

QY	1	CTCVPPHPQTAFCNSDLVIRAFVGTPEVNO-TTLYQ-----RYEIKMTKMYKGFQALG	53
DB	27	CSCSPVHPQQAFCNADVIRAKAVSEKVDSCNDIVGNPIKEIQYIKIMFK-----G	81
QY	54	DAADIRFVVTAPMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCSPVAPWNSLSLAQ	112
DB	82	PEKDIEFIYTAPSSAVCG-VSLDVGKKKEYLIAGRAEGDGKMHITLCDPFIVPWDTLSTTQ	140
QY	113	RRGFTKTYTVGCECTVPFCLSPCKLQSGTHCLWTDLQSGSEKGFQSRHLACLPREPG	172
DB	141	KKSLNHRVQMGCECKITRCPMIPCVISSPDECLWMDWVTEKNINGHOAKFPACIKRSDG	199
QY	173	LCTW	176
DB	200	SCAW	203

Search completed: December 17, 2002, 15:07:09
Job time : 19.4 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:26 ; Search time 10.1517 Seconds
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751.758 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1002	99.3	207	1	TIM1_PAPCY
3	989	98.0	207	1	TIM1_MACMU
4	893	88.5	207	1	TIM1_BOVIN
5	876	86.8	207	1	TIM1_SHEEP
6	866	85.8	207	1	TIM1_RIG
7	826	81.9	207	1	TIM1_HORSE
8	817.5	81.0	206	1	TIM1_RABIT
9	811	80.4	207	1	TIM1_CANFA
10	761.5	75.5	205	1	TIM1_MOUSE
11	742	73.5	217	1	TIM1_RAT
12	388.5	38.5	214	1	TIM3_SCYTO
13	383.5	38.0	220	1	TIM2_CHICK
14	382.5	37.9	220	1	TIM2_MOUSE
15	382.5	37.9	220	1	TIM2_RAT
16	381.5	37.8	212	1	TIM3_CHICK
17	380.5	37.7	220	1	TIM2_CAVPO
18	378.5	37.6	196	1	TIM2_CAVPO
19	378.5	37.6	214	1	TIM3_CRITIO
20	378.5	37.5	211	1	TIM3_XENLA
21	377.5	37.4	211	1	TIM3_HORSE
22	377.5	37.4	220	1	TIM3_HUMAN
23	374.5	37.1	220	1	TIM2_CANFA
24	373.5	37.0	211	1	TIM3_MOUSE
25	372.5	36.9	211	1	TIM3_RAT
26	370.5	36.7	220	1	TIM2_BOVIN
27	368.5	36.5	211	1	TIM3_BOVIN
28	363.5	36.0	194	1	TIM2_RABIT
29	360	35.7	224	1	TIM4_MOUSE
30	351	34.8	224	1	TIM4_HUMAN
31	350	34.7	224	1	TIM4_RAT
32	293.5	29.1	151	1	TIM3_RABIT
33	291	28.8	170	1	TIM4_RABIT

34	208	20.6	107	1	TIM4_BOVIN	O97563 bos taurus
35	158	15.7	210	1	TIMP_DROME	O97514 drosophila
36	146.5	14.5	91	1	TIM2_HORSE	O77717 equus caball
37	88.5	8.8	512	1	HYAL_MOUSE	P48794 mus musculus
38	78	7.7	535	1	PAH2_HUMAN	O15460 homo sapien
39	77.5	7.7	944	1	DNA4_YEAST	O08387 saccharomyc
40	76.5	7.6	183	1	DERM_BOVIN	P19427 bos taurus
41	75.5	7.5	423	1	YGCN_ECOLI	O46904 escherichia
42	75	7.4	461	1	TRIA_RAT	P22934 rattus norv
43	74.5	7.4	430	1	SVH_PORPU	P51348 porphyra pu
44	74.5	7.4	444	1	SKD1_MOUSE	P46467 mus musculus
45	73.5	7.3	444	1	SKD1_HUMAN	O75351 homo sapien

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	207 AA.
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AC	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid				
DE	potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases)				
DE	(Fibroblast collagenase inhibitor) (Collagenase inhibitor).				
CN	TIMP1 OR TIMP OR CLGI.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86040463; PubMed=3903517;				
RA	Docherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,				
RA	Harris T.J.R., Murphy G., Reynolds J.J.;				
RT	"Sequence of human tissue inhibitor of metalloproteinases and its				
RT	identity to erythroid-potentiating activity.";				
RL	Nature 318:66-69(1985).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86205964; PubMed=3010309;				
RA	Cartmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,				
RA	Welgus H.G., Stricklin G.P.;				
RT	"Primary structure and cDNA cloning of human fibroblast collagenase				
RT	inhibitor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Kaczmarek M., Honore N., Ribes V., Dehoux P., Cornet P., Cartwright T.,				
RA	Streck R.E.;				
RT	"Molecular cloning and synthesis of biologically active human tissue				
RT	inhibitor of metalloproteinases in yeast.";				
RL	Biotechnology 5:595-598(1987).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	TISSUE=Ovary;				
RX	MEDLINE=91025550; PubMed=2171551;				
RA	Rapp G., Freudenstein J., Klaidiny J., Mucha J., Wempe F., Zimmer M.,				
RA	Scheit K.H.;				
RT	"Characterization of three abundant mRNAs from human ovarian				
RT	granulosa cells.";				
RL	DNA Cell Biol. 9:479-485(1990).				

Nov 7.13.1985

Jun 1985

Nov 8/15/1985
priority to 4/5/1985

OY 181 SOIA 184
Db 204 SOIA 207

RESULT 2

TM1_PAPCY STANDARD; PRT; 207 AA.

AC P49061;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Metalloproteinase inhibitor 1 precursor (TIMP-1).

GN TIMP1.

OS Papio cynocephalus (Yellow baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Papio.

NCBI_TaxID=9556;

RP SEQUENCE FROM N.A.

RC TISSUE=Arteria;

RA MEDLINE=96011646; PubMed=7590279;

RA Forough R., Nikkari S.T., Hasenstab D., Lea H., Clowes A.W.;

RT "Cloning and characterization of a cDNA encoding the baboon tissue

inhibitor of matrix metalloproteinase-1 (TIMP-1).";

RL Gene 163:267-271(1995).

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)

CC AND IRREVERSIBLY INACTIVATES THEM.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF

DISULFIDE BONDS.

CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.

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CC -----

DR EMBL; L37295; AAA9943.1; -

DR HSSP; P01033; ID2B.

DR InterPro: IPR001820; TIMP.

DR Pfam; PF00965; TIMP; 1.

DR SMART; SM00206; TIMP; 1.

DR PROSITE; PS00288; TIMP; 1.

KM Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;

KM Signal.

FT CHAIN 1 23 BY SIMILARITY.

FT DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.

FT DISULFID 24 93 BY SIMILARITY.

FT DISULFID 26 122 BY SIMILARITY.

FT DISULFID 36 147 BY SIMILARITY.

FT DISULFID 150 197 BY SIMILARITY.

FT DISULFID 155 160 BY SIMILARITY.

FT DISULFID 168 189 BY SIMILARITY.

FT CARBOHYD 53 53 BY SIMILARITY.

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 207 AA; 23213 MW; 5AE4FDBEAB2ECDC CRC64;

Query Match 99.3%; Score 1002; DB 1; Length 207;

Best Local Similarity 98.9%; Pred. No. 1.1e-96;

Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTCVPHPHQTAFCNSDVIYRAKFGVTPVNOITLYQRYEIKTKTKYKGFQALGDAADIRF 60

Db 24 CTCVPHPHQTAFCNSDVIYRAKFGVTPVNOITLYQRYEIKTKTKYKGFQALGDAADIRF 83

OY 61 VYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHITTCSPVAPWNSLSLAORRGFTKTY 120

Db 84 VYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHITTCSPVAPWNSLSLAORRGFTKTY 143

OY 121 TWGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFOSRHLACLPRPGLCTWQSLR 180

Db 144 TWGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEKGFOSRHLACLPRPGLCTWQSLR 203

OY 181 SOIA 184
Db 204 TRIA 207

RESULT 3

TM1_MACMU STANDARD; PRT; 207 AA.

AC Q95KJ9;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Metalloproteinase inhibitor 1 precursor (TIMP-1).

GN TIMP1.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

NCBI_TaxID=9544;

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Ji S., Wang Y., Li H., Ji W., Piao Y.;

RT "Cloning and characterization of tissue inhibitor of matrix

metalloproteinase-1 (TIMP-1) cDNA from Macaca mulatta.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)

CC AND IRREVERSIBLY INACTIVATES THEM.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF

DISULFIDE BONDS.

CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.

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CC -----

DR EMBL; AF366397; AAK53704.1; -

DR InterPro: IPR001820; TIMP.

DR Pfam; PF00965; TIMP; 1.

DR PROSITE; PS00288; TIMP; FALSE NEG.

KM Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;

KM Signal.

FT CHAIN 1 23 BY SIMILARITY.

FT DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.

FT DISULFID 24 93 BY SIMILARITY.

FT DISULFID 26 122 BY SIMILARITY.

FT DISULFID 36 147 BY SIMILARITY.

FT DISULFID 150 197 BY SIMILARITY.

FT DISULFID 155 160 BY SIMILARITY.

FT DISULFID 168 189 BY SIMILARITY.

FT CARBOHYD 53 53 BY SIMILARITY.

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 207 AA; 23247 MW; 46E227D2AABA580 CRC64;

Query Match 98.0%; Score 989; DB 1; Length 207;

Best Local Similarity 97.8%; Pred. No. 2.4e-95;

Matches 180; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTCVPHPHQTAFCNSDVIYRAKFGVTPVNOITLYQRYEIKTKTKYKGFQALGDAADIRF 60

Db 24 CTCVPHPHQTAFCNSDVIYRAKFGVTPVNOITLYQRYEIKTKTKYKGFQALGDAADIRF 83

OY 61 VYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHITTCSPVAPWNSLSLAORRGFTKTY 120

```

Db 84 VYTPAMESVCGYFHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSLAQRGGFTKTY 143
Qy 121 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGKEGFSQSRHLACLPRPGLCTWQSLR 180
Db 144 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGKEGFSQSRHLACLPRPGLCTWQSLR 203
Qy 181 SQIA 184
Db 204 TRMA 207

RESULT 4
TIM1_BOVIN STANDARD; PRT; 207 AA.
AC P20414; Q9TVB0;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-1).
GN TIMP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RX MEDLINE=90365711; PubMed=2393392;
RA Freudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.; "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue.";
RL Biochem. Biophys. Res. Commun. 171:250-256 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94257757; PubMed=8199264;
RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.; "Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct cells enhances in vitro development of bovine embryo.";
RL Biol. Reprod. 50:835-844 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94257757; PubMed=8199264;
RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.; "Involvement of fibroblasts and muscle cells in the expression of an extracellular proteolytic cascade in bovine skeletal muscle.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 24-69.
RX MEDLINE=90008914; PubMed=2551303;
RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.; "Purification and characterization of two related but distinct metalloproteinase inhibitors secreted by bovine aortic endothelial cells.";
RL J. Biol. Chem. 264:17445-17453 (1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
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CC -----
CC EMBL; M60073; AAA30784.1; -.

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DR EMBL; S70841; AAB30892.1; -.
DR EMBL; AF144763; AAD30303.1; -.
DR PIR; A35685; A35685.
DR PIR; B34468; B34468.
DR HSP; P01033; IUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00286; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation; Signal.
FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
FT CHAIN 24 207 BY SIMILARITY.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 207 AA; E672BEE2E865F3F7 CRC64;

Query Match 88.5%; Score 893; DB 1; Length 207;
Best Local Similarity 87.0%; Pred. No. 21e-85;
Matches 160; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDLVIRAKFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83
Qy 61 VYTAMESVCGYFHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSLAQRGGFTKTY 120
Db 84 IYTPAMESVCGYFHRSHNRSEEFLLAGLQGLLHITTCFVAPWNSLSLAQRGGFTKTY 143
Qy 121 TVGCECTVFPCLSPCKLQSGTHCLWTDQLQSGKEGFSQSRHLACLPRPGLCTWQSLR 180
Db 144 AAGCECTVFPCLSPCKLQSGTHCLWTDQLQSGKEGFSQSRHLACLPRPGLCTWQSLR 203
Qy 181 SQIA 184
Db 204 AQMA 207

RESULT 5
TIM1_SHEEP STANDARD; PRT; 207 AA.
AC P50122;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
ON NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Corpus luteum; MEDLINE=94102210; PubMed=8275949;
RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.; "Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: ontogeny of messenger ribonucleic acid expression and in situ localization within preovulatory follicles and luteal tissue.";
RL Endocrinology 134:344-352 (1994).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
CC -----

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CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 CC -----
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 CC EMBL; S67450; AAB29472.1; -
 CC HSSP; P01033; IUBA.
 CC InterPro; IPR001820; TIMP.
 CC Pfam; PF00965; TIMP; 1.
 CC SMART; SM00206; TIMP; 1.
 CC PROSITE; PS00288; TIMP; 1.
 CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 CC Signal.
 CC CHAIN 1 23 BY SIMILARITY.
 CC SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
 CC CHAIN 24 207 BY SIMILARITY.
 CC DISULFID 24 93 BY SIMILARITY.
 CC DISULFID 26 122 BY SIMILARITY.
 CC DISULFID 36 147 BY SIMILARITY.
 CC DISULFID 150 197 BY SIMILARITY.
 CC DISULFID 155 160 BY SIMILARITY.
 CC DISULFID 168 189 BY SIMILARITY.
 CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 207 AA; 23057 MW; 1DBCA2012F80E46 CRC64;
 SO
 Query Match 86.8%; Score 876; DB 1; Length 207;
 Best Local Similarity 86.7%; Pred. No. 1,2e-83;
 Matches 156; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 CTCVPHQOTAFCSNDLYIRAKFGTPEVNOTLYQRYEIKMTKMYKGFQALGDAADIRF 60
 DB 24 CTCVPHQOTAFCSNDLYIRAKFGTPEVNOTLYQRYEIKMTKMYKGFQALGDAADIRF 83
 QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKY 120
 DB 84 IYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKY 143
 QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGEKFGFQSHLACLPRPGLCTWQSLR 180
 DB 144 AAGCECTVFPCLSPCKLQSGTHCLMTDQLQSGEKFGFQSHLACLPRPGLCTWQSLR 203
 F. T 6
 T. PIG
 ID -TIM1_PIG STANDARD: PRT; 207 AA.
 AC P35624; O9T83; O9T89;
 DT 01-JUN-1994 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Metalloprotease inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID:9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE:Ovary;
 RX MEDLINE=92201478; PubMed=1312961;
 RA Tanaka T., Andoh N., Takeya T., Sato E.;
 RT "Differential screening of ovarian cDNA libraries detected the
 RT expression of the porcine collagenase inhibitor gene in functional
 RT corpora lutea."
 RL Mol. Cell. Endocrinol. 83:65-71(1992).
 RP SEQUENCE OF 34-195 FROM N.A.
 RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
 RT "Gene expression level of mmp3 and Timp1 in intervertebral disc.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 37-144 FROM N.A.
 RC TISSUE-Skin;
 RA Wang J.F., Boykiv R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine Timp1."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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 CC EMBL; S96211; AAB21865.1; -
 CC EMBL; AF201726; AAF24348.1; -
 CC EMBL; AF156029; AAF17354.1; -
 CC HSSP; P01033; IUBA.
 CC InterPro; IPR001820; TIMP.
 CC Pfam; PF00965; TIMP; 1.
 CC SMART; SM00206; TIMP; 1.
 CC PROSITE; PS00288; TIMP; 1.
 CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 CC Signal.
 CC CHAIN 1 23 BY SIMILARITY.
 CC SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
 CC CHAIN 24 207 BY SIMILARITY.
 CC DISULFID 24 93 BY SIMILARITY.
 CC DISULFID 26 122 BY SIMILARITY.
 CC DISULFID 36 147 BY SIMILARITY.
 CC DISULFID 150 197 BY SIMILARITY.
 CC DISULFID 155 160 BY SIMILARITY.
 CC DISULFID 168 189 BY SIMILARITY.
 CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 34 34 A -> P (IN REF. 2).
 CC CONFLICT 37 37 S -> N (IN REF. 3).
 CC CONFLICT 41 41 V -> F (IN REF. 2).
 CC CONFLICT 43 43 K -> Q (IN REF. 1).
 CC CONFLICT 59 59 T -> A (IN REF. 3).
 CC CONFLICT 86 86 EI -> KT (IN REF. 3).
 CC SEQUENCE 207 AA; 23098 MW; B04895846EB56BD0 CRC64;
 SQ
 Query Match 85.8%; Score 866; DB 1; Length 207;
 Best Local Similarity 83.2%; Pred. No. 1,3e-82;
 Matches 153; Conservative 14; Mismatches 17; Indels 0; Gaps 0;
 QY 1 CTCVPHQOTAFCSNDLYIRAKFGTPEVNOTLYQRYEIKMTKMYKGFQALGDAADIRF 60
 DB 24 CTCVPHQOTAFCSNDLYIRAKFGTPEVNOTLYQRYEIKMTKMYKGFQALGDAADIRF 83
 QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKY 120
 DB 84 IYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSPVAPNNSLSLAQRGFTKY 143
 QY 121 TVGCECTVFPCLSPCKLQSGTHCLMTDQLQSGEKFGFQSHLACLPRPGLCTWQSLR 180
 DB 144 AAGCECTVFPCLSPCKLQSGTHCLMTDQLQSGEKFGFQSHLACLPRPGLCTWQSLR 203
 QY 181 SQIA 184
 DB 204 PRVA 207
 RESULT 7
 TIM1_HORSE

```

ID TIM1_HORSE STANDARD; PRT; 207 AA.
AC O02722;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA MEDLINE=99074117; PubMed=9858406;
RA Richardson D.W., Dodge G.R.;
RT "Molecular characteristics of equine stromelysin and the tissue
inhibitor of metalloproteinase 1";
RL Am. J. Vet. Res. 59:1557-1562(1998).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC
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CC
CC EMBL; U95039; AAB53735.1;
DR HSSP; P01033; LUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23046 MW; FD710DA98D168070 CRC64;

Query Match 81.9%; Score 826; DB 1; Length 207;
Best Local Similarity 82.1%; Pred. No. 1.9e-78;
Matches 151; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPQTAFCSSEFVIRAKFVGTSVNTTLYQRYEIKTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVFPCLSPCKLQSDTCLWTDLQGLQSEKGFQSRHLACLPRPGCLTQWSLR 180
DB 144 AAGCECSVFPCLSPCKLQSDTCLWTDLQGLQSEKGFQSRHLACLPRPGCLTQWSLR 203
QY 181 SOIA 184
DB 204 PRTA 207

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RESULT 8
TIM1_RABBIT STANDARD; PRT; 206 AA.
AC P20614;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89214135; PubMed=2708356;
RA Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H.,
RA Quible D.J.;
RT "Hyperoxic exposure alters gene expression in the lung. Induction of
the tissue inhibitor of metalloproteinases mRNA and other mRNAs.";
RL J. Biol. Chem. 264:7092-7095(1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J04712; AAA31478.1;
DR PIR; A33350; A33350.
DR HSSP; P01033; ID2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 206 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 196 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 188 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 206 AA; 22758 MW; 1839A8DE7174EE9E CRC64;

Query Match 81.0%; Score 817.5; DB 1; Length 206;
Best Local Similarity 81.7%; Pred. No. 1.4e-77;
Matches 147; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 1 CTCVPPHPQTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPQTAFCSNDLVIRAKFVGTPVNTTLYQRYEIKTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 120
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAQRGFTKTY 143
QY 121 TVGCECTVFPCLSPCKLQSDTCLWTDLQGLQSEKGFQSRHLACLPRPGCLTQWSLR 180

```

DB 144 AACGCMCTVACASIPCHESDTHCLMTDSSL-GSDKGQSHHACLPOEPGLCMESLR 202

RESULT 9

TIM1_CANFA STANDARD: PRT: 207 AA.

ID TIM1_CANFA STANDARD: PRT: 207 AA.

AC P81546; Q9TQ55; Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Metalloprotease inhibitor 1 precursor (TIMP-1).

GN TIMP1.

OS Caris familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=MADIN-DURBY;

RA Noritake H., Miyamori H., Goto C., Seiki M., Sato H.;

RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=99132652; PubMed=9931441;

RA Zeiss C.U., Acland G.M., Aguirre G.D., Ray K.;

RT "TIMP-1 expression is increased in X-linked progressive retinal atrophy despite its exclusion as a candidate gene.;"

RL Gene 225:67-75(1998).

RN [3]

RP CHARACTERIZATION.

RA MEDLINE=92175241; PubMed=1794505;

RA Chopra R., Kokilic P.A., Bergin S., Rowe J., Angal S.;

RT "Purification of recombinant dog tissue inhibitor of metalloproteinases.;"

RL Biochem. Soc. Trans. 19:372S-372S(1991).

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HIGHEST IN KIDNEY AND OVARY.

CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.

CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.

CC -----

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CC -----

DR EMBL; AB016817; BAA3293.1; -

DR EMBL; AF077817; AAD10632.1; -

DR EMBL; AF079767; AAD10633.1; -

DR HSSP; P01033; IUBA.

DR InterPro: IPR001820; TIMP.

DR Pfam; PF00965; TIMP.1.

DR SMART; SM00206; TIMP.1.

DR PROSITE; PS00288; TIMP; FALSE_NEG.

KM Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation; signal.

KM SIGNAL.

FT CHAIN 1 23 BY SIMILARITY.

FT DISULFID 24 207 METALLOPROTEINASE INHIBITOR 1.

FT DISULFID 26 122 BY SIMILARITY.

FT DISULFID 36 147 BY SIMILARITY.

FT DISULFID 150 197 BY SIMILARITY.

FT DISULFID 155 160 BY SIMILARITY.

FT DISULFID 168 189 BY SIMILARITY.

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 17 17 V -> L (IN REF. 1).

FT CONFLICT 35 35 L -> F (IN REF. 1).

FT CONFLICT 173 173 H -> Q (IN REF. 1).

FT CONFLICT 203 203 MISSING (IN REF. 1).

SO SEQUENCE 207 AA: 22852 MW; D36C8A67BB3B784D CXC64;

Query Match 80.4%; Score 811; DB 1; Length 207;

Best Local Similarity 79.3%; Pred. No. 6,7e-77;

Matches 146; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 1 CTCVPPHQATFACNSDLYIRAKFVGTPEVNOITLYQREIKMTKYKGFQALGDAADIRF 60

DB 24 CTCAPPHQATFACNSQIVIRAKFVGTAEVNOITLYRREIKMTKYKGFSAAGNASDIRF 83

QY 61 VTPAMESVCGYFPHSRSHRSEFFLAGLQDGLHITTCSPFAPNLSLQRRGFTKTY 120

DB 84 VTPALBSVCGYLNRSQNRSEFFLVAGNLRDGLINTCSFVAPNLSLSTQRRGFTKTY 143

QY 121 TVGCECTVFPCLSPCKLQSGTCHLMTDOLQSEKGFQSHHACLPREPGLCTWQSLR 180

DB 144 AACGCMCTVACASIPCHESDTHCLMTDSSL-GSDKGQSHHACLPOEPGLCMESLR 203

QY 181 SCIA 184

DB 204 PRMA 207

RESULT 10

TIM1_MOUSE STANDARD: PRT: 205 AA.

ID TIM1_MOUSE STANDARD: PRT: 205 AA.

AC P12032; P20064;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Metalloprotease inhibitor 1 precursor (TIMP-1) (Erythroid potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Collagenase inhibitor 16C8 fibroblast) (TPA-induced protein) (TPA-SI).

GN TIMP1 OR TIMP-1 OR TIMP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=87218524; PubMed=3034603;

RA Gewert D.R., Coulombe B., Castellino M., Skup D., Williams B.R.G.;

RT "Characterization and expression of a murine gene homologous to human EPA/TIMP: a virus-induced gene in the mouse.;"

RL EMBO J. 6:651-657(1987).

RN [2]

RP SEQUENCE FROM N.A.

RA TISSUE=Fibroblast;

RC MEDLINE=87066763; PubMed=3024122;

RA Edwards D.R., Waterhouse P., Holman M.L., Denhardt D.T.;

RT "A growth-responsive gene (16C8) in normal mouse fibroblasts homologous to a human collagenase inhibitor with erythroid-potentiating activity: evidence for inducible and constitutive transcripts.;"

RL Nucleic Acids Res. 14:8863-8878(1986).

RN [3]

RP SEQUENCE FROM N.A.

RA STRAIN=C3H;

RC MEDLINE=86038821; PubMed=3670294;

RA Johnson M.D., Housey G.M., Kirschmeier P.T., Weinstein I.B.;

RT "Molecular cloning of gene sequences regulated by tumor promoters and mitogens through protein kinase C.;"

RL Mol. Cell. Biol. 7:2821-2829(1987).

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIETIS IN VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID PROGENITORS.

CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- TISSUE SPECIFICITY: FOUND IN FETAL AND ADULT TISSUES. HIGHEST
CC LEVELS ARE FOUND IN BONE. ALSO FOUND IN LUNG, OVARY AND UTERUS.
CC -1- INDUCTION: REGULATED BY TUMOR PROMOTERS AND MITOGENS THROUGH
CC PROTEIN KINASE C. ALSO INDUCED BY VIRUSES.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC
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CC
CC EMBL; M28312; AAB42179.1; -
CC EMBL; M28308; AAB42179.1; JOINED.
CC EMBL; M28309; AAB42179.1; JOINED.
CC EMBL; M28310; AAB42179.1; JOINED.
CC EMBL; M28311; AAB42179.1; JOINED.
CC EMBL; X04684; CRA28387.1; -
CC EMBL; M17243; AAB40471.1; -
CC PIR; A26633; A26633.
CC PIR; A26106; A26106.
CC PIR; A26917; A26917.
CC HSSP; P01033; 1UEA.
CC MGD; MGI:98752; Timp.
CC InterPro; IPR001820; TIMP.
CC Pfam; PF00965; TIMP; 1.
CC SMART; SM00206; TIMP; 1.
CC PROSITE; PS00288; TIMP; 1.
CC Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
CC KW
CC Signal.
CC
CC CHAIN 1 24 METALLOPROTEINASE INHIBITOR 1.
CC DISULFID 25 205 BY SIMILARITY.
CC DISULFID 25 94 BY SIMILARITY.
CC DISULFID 27 123 BY SIMILARITY.
CC DISULFID 37 148 BY SIMILARITY.
CC DISULFID 151 197 BY SIMILARITY.
CC DISULFID 156 161 BY SIMILARITY.
CC DISULFID 169 189 BY SIMILARITY.
CC CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 52 52 E -> R (IN REF. 1).
CC CONFLICT 66 66 M -> MM (IN REF. 1).
CC CONFLICT 117 118 NL -> KF (IN REF. 1).
CC CONFLICT 121 121 S -> N (IN REF. 1).
CC CONFLICT 139 139 A -> V (IN REF. 1).
CC CONFLICT 143 143 T -> KN (IN REF. 1).
CC CONFLICT 194 194 P -> L (IN REF. 1).
CC SEQUENCE 205 AA; 22628 MW; FAC952D49A50FD7 CRC64;
Query Match 75.5%; Score 761.5; DB 1; Length 205;
Best Local Similarity 73.7%; Pred. No. 9e-72;
Matches 132; Conservative 25; Mismatches 21; Indels 1; Gaps 1;
Qy 1 CTCVPHPTACNSDLVIRAKFVGTPEVNOTTLVORVEIKMTKMYKGFOALGDAADIRF 60
Db 25 CSCAPHPPTACNSDLVIRAKFVGTPEVNOTTLVORVEIKMTKMYKGFOALGDAADIRF 84
Qy 61 VYTPAMESVCGYFHRSHNRSEBFLIAGLQDLGLHITTCSPVAPNWSLSAQRGGFTKTY 120
Db 85 AYTPTWESLCGYAHKSNQSEBFLITGLRNLGNLHISACSLFVPTLTSPAQRAFSTKY 144
Qy 121 TVGCECTVPCSLIPCKLQSGTHCLWTDLQGLQSGKEGFSQSHLACLPRPGLCTWQSL 179
Db 145 SAGCGVCTVFPCLSPCKLESHTCLWTDLQGLVSGSE-DYQSRHFACLPENPGLCTWRS 202
RESULT 11
TIMP_RAT

ID AC TIMP_RAT STANDARD; PRT; 217 AA.
DT P30120; P70533;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1 OR TIMP-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skin dorsal;
RX MEDLINE=95011636; PubMed=7926820;
RA Okada A., Garnier J.M., Vicaire S., Basset P.;
RT "Cloning of the cDNA encoding rat tissue inhibitor of
RT metalloproteinase 1 (TIMP-1), amino acid comparison with other TIMPs,
RT and gene expression in rat tissues.";
RL Gene 147:301-302(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX Gibbons K.L., O'Grady R.L., Piper A.A.;
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 30-205 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96317624; PubMed=8707259;
RA Iredale J.P., Benyon R.C., Arthur M.J.P., Ferris W.F., Alcolado R.,
RA Winwood P.J., Clark N., Murphy G.;
RT "Tissue inhibitor of metalloproteinase-1 messenger RNA expression is
RT enhanced relative to interstitial collagenase messenger RNA in
RT experimental liver injury and fibrosis.";
RL Hepatology 24:176-184(1996).
RN [4]
RP SEQUENCE OF 39-156 FROM N.A., SEQUENCE OF 24-38, INDUCTION, FUNCTION,
RP AND SUBCELLULAR LOCATION.
RX STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;
RX MEDLINE=95296691; PubMed=777858;
RA Boujrad N., Ogwegu S.O., Garnier M., Lee C.-H., Martin B.M.,
RA Papadopoulos V.;
RT "Identification of a stimulator of steroid hormone synthesis isolated
RT from testis.";
RL Science 268:1609-1612(1995).
RN [5]
RP SEQUENCE OF 24-45.
RX MEDLINE=92117648; PubMed=1309971;
RA Roswit W.T., McCourt D.W., Partridge N.C., Jeffrey J.J.;
RT "Purification and sequence analysis of two rat tissue inhibitors of
RT metalloproteinases.";
RL Arch. Biochem. Biophys. 292:402-410(1992).
CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC and irreversibly inactivates them. Also stimulates steroidogenesis
CC by Leydig and ovarian granulosa cells; procathepsin L is required
CC for maximal activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- INDUCTION: By follicle-stimulating hormone (FSH).
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC
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CC
CC EMBL; U06179; AAA85780.1; -
CC EMBL; L31883; AAA85373.1; -
CC EMBL; L29512; AAB08483.1; -

DR EMBL; U16022; AAA51653.1; ALT_SEQ.
 DR PIR; S20326; S20326.
 DR HSSP; P01033; IUEA.
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR PROSITE; PS00206; TIMP; 1.
 DR PROSITE; PS00288; TIMP; 1.
 DR Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 KW Steroidogenesis; Signal.
 KM SIGNAL
 FT CHAIN 1 23
 FT DISULFID 24 217 METALLOPROTEINASE INHIBITOR 1.
 FT DISULFID 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 197 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.
 FT DISULFID 168 189 BY SIMILARITY.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 80 81 GP -> DI (IN REF. 3).
 FT CONFLICT 88 88 A -> V (IN REF. 4).
 FT CONFLICT 103 103 S -> R (IN REF. 3).
 FT CONFLICT 129 130 HN -> AS (IN REF. 3).
 FT CONFLICT 136 140 OKAFV -> RKGLT (IN REF. 3).
 FT CONFLICT 149 149 V -> L (IN REF. 4).
 FT CONFLICT 157 157 A -> V (IN REF. 3).
 FT CONFLICT 166 166 S -> T (IN REF. 3).
 FT CONFLICT 185 187 DHF -> RHL (IN REF. 3).
 FT CONFLICT 195 195 D -> G (IN REF. 3).
 FT CONFLICT 201 201 Y -> S (IN REF. 3).
 FT CONFLICT 204 205 VS -> SR (IN REF. 3).
 FT SEQUENCE 217 AA; 23793 MW; C5AC240A61C1A1DF CRC64;

Query Match 73.5%; Score 742; DB 1; Length 217;
 Best Local Similarity 71.5%; Pred. No. 1e-69;
 Matches 128; Conservative 23; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCVPPHPOTACNSDLYIRAKFVGTPEVNOFTLYORYEIKMTKWKYKGQALGDADIRF 60
 DB 24 CSCAPHPPTACNSDLYIRAKFMSPEIETTLVORYEIKMTKMKGDVAGNATGFRF 83
 QY 61 YVTPAMESVCGYFHRSHNSEEFLLAGKLQDGLHLITTCGFPVAPWNSLSLAQRGFTKT 120
 DB 84 AYTPAMESLCGYVHKSHNSSEFLLAGRLRNGLNHLITACSPFLVPMNLSLPAQKAFVKTY 143
 QY 121 YVGCCECTVFPCLSIPTCKLQSGTHCLMTDQLLOGSEKGFQSRHLACLPRPGLCTWQSL 179
 DB 144 SAGCGVCTVFPCLSIPTCKLQSGTHCLMTDQILMGSEKGYQSDHFACTLPNPDLCWQYL 202
 RESULT 12
 TIM3_SCYTO
 ID TIM3_SCYTO STANDARD; PRT; 214 AA.
 AC Q9W6B4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metalloprotease inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of
 DE metalloproteinases-3).
 GN TIMP3.
 OS Scyliorhinus torazame (Cloudy catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 NC NCB1_TaxID=75743;
 NX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Cartilage;
 RX PubMed=11342115;
 RA Kim J.-T., Kim M.-S., Bae M.-K., Song H.S., Ahn M.-Y., Kim Y.-J.,
 RA Lee S.-J., Kim K.-W.,
 RA "Cloning and characterization of tissue inhibitor of
 RT metalloproteinase-3 (TIMP-3) from shark, Scyliorhinus torazame.";

RL Biochim. Biophys. Acta 1517:311-315(2001).
 CC - FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM. MAY FORM PART OF A TISSUE-
 CC SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI (By similarity).
 CC - SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By
 CC similarity).
 CC - TISSUE SPECIFICITY: Expressed abundantly in brain and cartilage.
 CC - SIMILARITY: BELONGS TO THE TIMP FAMILY.
 CC
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DR EMBL; AF110767; AAD26150.1; .
 DR HSSP; P16035; 2TMP.
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR PROSITE; PS00288; TIMP; 1.
 DR Metalloprotease inhibitor; Signal.
 KM SIGNAL
 FT CHAIN 1 26
 FT DISULFID 27 214 METALLOPROTEINASE INHIBITOR 3.
 FT DISULFID 29 94 BY SIMILARITY.
 FT DISULFID 29 121 BY SIMILARITY.
 FT DISULFID 39 146 BY SIMILARITY.
 FT DISULFID 148 195 BY SIMILARITY.
 FT DISULFID 153 158 BY SIMILARITY.
 FT DISULFID 166 187 BY SIMILARITY.
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 214 AA; 24498 MW; BCAD3008BE4B3557 CRC64;

Query Match 38.5%; Score 388.5; DB 1; Length 214;
 Best Local Similarity 40.1%; Pred. No. 4.4e-33;
 Matches 71; Conservative 32; Mismatches 67; Indels 7; Gaps 4;

QY 1 CTCVPPHPOTACNSDLYIRAKFVGTPEVNOFTLYORYEIKMTKWKYKGQALGDADIR 59
 DB 27 CTCWNNHPOEAFNCNSDLYIRAKVGGKLLKDGPGCTMRYYTIKQMKMYGFGSKM--QQVQ 83
 QY 60 FYVTPAMESVCGYFHRSHNSEEFLLAGKLQDGLHLITTCGFPVAPWNSLSLAQRGFTKT 119
 DB 84 YVTPAMESVCGYFHRSHNSEEFLLAGKLQDGLHLITTCGFPVAPWNSLSLAQRGFTKT 141
 QY 120 YVGCCECTVFPCLSIPTCKLQSGTHCLMTDQLLOGSEKGFQSRHLACLPRPGLCTW 176
 DB 142 YQYGC-NCKIKRCYLLPCFVIRAKNCEFTDMLSDQGVNGHAKYVVCIRQKRGYCSW 197

RESULT 13
 TIM2_CHICK
 ID TIM2_CHICK STANDARD; PRT; 220 AA.
 AC O42146;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Metalloprotease inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
 DE metalloproteinases-2).
 GN TIMP2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9031;
 NX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=96122528; PubMed=9462696;
 RX Aimes R.T., Li L.H., Weaver B., Hawkes S., Hahn-Dantona E.A.,
 RA Outgley J.P.;
 RA "Cloning, expression, and characterization of chicken tissue


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Db 141 KSLNHRQMG-C-ECKITRCPMIPYISSPDECLMMDWTEKSIHQAKFPACIKRSDG 199
Oy 173 LCTW 176
Db 200 SCAM 203

RESULT 15
TIM2_RAT
ID _TIM2_RAT STANDARD: PRT: 220 AA.
AC P30121.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2).
GN TIMP2 OR TIMP-2.
OC Rattus norvegicus (Rat).
OC Sukariycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Bone;
RA MEDLINE=94263207; PubMed=8203893;
RX Cook T.F., Burke J.S., Bergman K.D., Quinn C.O., Jeffrey J.J.,
RA Partridge N.C.;
RT "Cloning and regulation of rat tissue inhibitor of
RT metalloproteinases-2 in osteoblastic cells.";
RL Arch. Biochem. Biophys. 311:313-320(1994).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Gibbons K.L., O'Grady R.L., Piper A.A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA MEDLINE=94326839; PubMed=8050496;
RX Sanctoro M., Battaglia C., Zhang L., Carlomagno F., Martelli M.L.,
RA Salvatore D., Fusco A.;
RT "Cloning of the rat tissue inhibitor of metalloproteinases type 2
RT (TIMP-2) gene: analysis of its expression in normal and transformed
RT thyroid cells.";
RL Exp. Cell Res. 213:398-403(1994).
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=96384329; PubMed=8792217;
RX Grima J., Calciagno K., Cheng C.Y.;
RT "Purification and sequence analysis of two rat tissue inhibitors of
RT metalloproteinases.";
RL Arch. Biochem. Biophys. 292:402-410(1992).
-1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U14526; AAA81553.1; -
DR EMBL: L31884; AAA84581.1; -
DR EMBL: S72594; AAC60687.1; -
DR EMBL: S82718; AAB49507.1; -
DR PIR: S20325; S20325.
DR HSSP: P16035; 1BR9.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP.1.
DR SMART: SM00206; TIMP.1.
DR PROSITE: PS00288; TIMP.1.
KW Metalloproteinase inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
FT CONFLICT 7 7 S->T (IN REF. 1).
FT CONFLICT 153 153 E->Q (IN REF. 1).
SQ SEQUENCE 220 AA; 24356 MW; 1C97A3F050C3AETD CRC64;

Query Match 37.9%; Score 382.5; DB 1; Length 220;
Best Local Similarity 41.8%; Pred. No. 1.9e-32;
Matches 77; Conservative 27; Mismatches 65; Indels 15; Gaps 6;

Oy 1 CTGVPHPTQAFCSNDSLVIRAKFVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53
Db 27 CSCSPVHPQAFQCNADVIRAKAVEKEVDGNDYGNPIRIQYEIKQIKFK-----G 81
Oy 54 DAADIRFYVTPAMESVCGYFHRSHNRSEFPIAGKQ-DGLHITTCSPVAPWNSLSLAQ 112
Db 82 PDKDIEFLYTPASSAVCG-VSLDVGGKKEYIAGKABGDGMHITLCPFIWMDLSITQ 140
Oy 113 RRGFTKTVTGCEECTVPPCLSPCKLGGTHCLWTDLLOGSEKGFQSRHLACLPBPG 172
Db 141 KSLNHRQMG-C-ECKITRCPMIPYISSPDECLMMDWTEKSIHQAKFPACIKRSDG 199
Oy 173 LCTW 176
Db 200 SCAM 203

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Search completed: December 17, 2002, 15:04:52
Job time : 11.1517 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 33.6276 Seconds
(without alignments)
1127.428 Million cell updates/sec

Title: US-09-452-817-1

Perfect score: 1009
Sequence: 1 CTCVPHPHQTAFCNSDLVIR.....ACLPREPGLCTWQSLRSQIA 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	800	79.3	169 4 Q96QM2	Q96QM2 homo sapien
2	633	62.7	137 6 Q9M212	Q9M212 ovis aries
3	515	51.0	145 11 Q912P7	Q912P7 rattus norv
4	368.5	36.5	11 Q925O6	Q925O6 mus muscricetu
5	297.5	29.5	152 6 Q9T7B6	Q9T7B6 sus scrofa
6	282	27.9	170 6 Q9T7B6	Q9T7B6 sus scrofa
7	246.5	24.4	138 6 Q9T7B6	Q9T7B6 sus scrofa
8	232.5	23.0	126 6 Q9T7B6	Q9T7B6 sus scrofa
9	188.5	18.7	97 6 Q95KL7	Q95KL7 macaca mulia
10	181.5	18.0	221 5 Q96PJ2	Q96PJ2 crassostrea
11	149.5	14.8	38 11 Q61720	Q61720 mus musclicu
12	129.5	12.8	97 13 Q8UW9	Q8UW9 xenopus lae
13	124	12.3	25 11 Q9QV13	Q9QV13 rattus sp.
14	124	12.3	25 11 Q9QV13	Q9QV13 mus sp. col
15	106.5	10.6	280 5 Q962H0	Q962H0 cucumaria f
16	106	10.5	30 11 Q9QV14	Q9QV14 mus sp. col

17	88.5	8.8	512 11 Q9DAQ1	Q9DAQ1 mus musclicu
18	83.5	8.3	187 5 Q9NDF1	Q9NDF1 heterodera
19	83	8.2	4307 5 Q19319	Q19319 caenorhabdi
20	79.5	7.9	1062 5 Q19204	Q19204 caenorhabdi
21	79	7.8	682 10 Q9L7E3	Q9L7E3 arabidopsis
22	77.5	7.7	701 11 Q92312	Q92312 mus musclicu
23	76.5	7.6	626 10 Q9FXY0	Q9FXY0 arabidopsis
24	76	7.5	340 3 Q9P3W4	Q9P3W4 schizosacch
25	75.5	7.5	257 16 Q932H6	Q932H6 staphylococ
26	75.5	7.5	530 10 Q80793	Q80793 arabidopsis
27	75.5	7.5	1106 13 Q42291	Q42291 gallus gall
28	75.5	7.5	1513 11 Q62635	Q62635 rattus norv
29	74.5	7.4	263 10 Q9AVH5	Q9AVH5 pistum sativ
30	74.5	7.4	444 11 Q91W22	Q91W22 mus musclicu
31	74.5	7.4	1326 4 Q9P219	Q9P219 homo sapien
32	74	7.3	158 5 Q21265	Q21265 caenorhabdi
33	74	7.3	1006 12 Q85064	Q85064 peanut stum
34	74	7.3	1179 5 Q9NBM4	Q9NBM4 trypanosoma
35	73.5	7.3	444 4 Q9GZ57	Q9GZ57 homo sapien
36	73.5	7.3	1963 4 Q75051	Q75051 homo sapien
37	73	7.2	555 10 Q23590	Q23590 arabidopsis
38	73	7.2	993 12 Q8UYT4	Q8UYT4 tomato aspe
39	73	7.2	3132 12 Q9QW08	Q9QW08 japanese ya
40	72.5	7.2	225 5 Q27013	Q27013 tenedrio mo
41	72.5	7.2	225 5 Q27014	Q27014 tenedrio mo
42	72.5	7.2	425 12 Q68393	Q68393 human cytom
43	72.5	7.2	517 4 Q75294	Q75294 homo sapien
44	72.5	7.2	611 16 Q9KAS8	Q9KAS8 bacillus ha
45	72	7.1	109 4 Q13058	Q13058 homo sapien

ALIGNMENTS

RESULT 1

Q96QM2 PRELIMINARY; PRT; 169 AA.
AC Q96QM2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (erythroid potentiating
DE activity, collagenase inhibitor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Straubeberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007097; AA07097.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; UNKNOWN 1.
SQ SEQUENCE 169 AA; 18847 MW; EC164206C87D815C CRC64;

Query Match 79.3%; Score 800; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 8e-80;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCVPHPHQTAFCNSDLVIRAKFVGTPEVNOTTLYOREIKMTKYKGFQALGDAADIRF	60
DB	24	CTCVPHPHQTAFCNSDLVIRAKFVGTPEVNOTTLYOREIKMTKYKGFQALGDAADIRF	83
QY	61	VYTPMBSVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLQRRGFTYTY	120
DB	84	VYTPMBSVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSEFVAPWNSLSLQRRGFTYTY	143
QY	121	TVGCECTVFPCLSTPCKLQSGTHTCL	146
DB	144	TVGCECTVFPCLSTPCKLQSGTHTCL	169

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RESULT 2
Q9M212
ID Q9M212 PRELIMINARY; PRT; 137 AA.
AC Q9M212;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347710; PubMed=10888873;
RA Galloway S.M., McNatty K.P., Cambridge L.M., Laitinen M.P.E.,
RA Juengel J.L., Jokiranta S., McLaren R.J., Luiro K., Dodds K.D.,
RA Montgomery G.W., Beattie A.E., Davis G.H., Ritvos O.;
RA "Mutations in an oocyte-derived growth factor (BMP15) cause increased
RT ovulation rate and infertility in a dosage-sensitive manner.";
RL Nat. Genet. 25:279-283(2000).
DR EMBL; AF268477; AAF81746.1; -.
DR HSSP; P01033; 1D2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15396 MW; 62009B069D0594B7 CRC64;

Query Match 62.7%; Score 633; DB 6; Length 137;
Best Local Similarity 84.7%; Pred. No. 1.3e-61;
Matches 116; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 7 HPOTAFCSNLDVIRAKFVGTPVNOTTLVYRIEIKMTKMYKGFQALGDAADIRFVYTPAM 66
Db 1 HPOTAFCSNLDVIRAKFVGTPVNOTTLVYRIEIKMTKMYKGFQALGDAADIRFVYTPAM 60

QY 67 ESVCCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAORRGFTKTYTGCEE 126
Db 61 ESVCCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAORRGFTKTYTGCEE 120

QY 127 CTVFPCLSPCKLQSGT 143
Db 121 CTVFPCLSPCKLQSGT 137

RESULT 3
Q91ZP7
ID Q91ZP7 PRELIMINARY; PRT; 145 AA.
AC Q91ZP7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=OVARY;
RA Espey L.L., Ujioka T., Okamura H., Richards J.S.;
RA "Expression of metallothionein-1 (MT-1) in steroid-secreting cells of
RT the rat ovary during the peri-ovulatory period following gonadotropin
RT treatment.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411319; AAL05862.1; -.
DR InterPro; IPR001820; TIMP.
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DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
SQ SEQUENCE 145 AA; 15954 MW; 7EC7053DA82DE913 CRC64;

Query Match 51.0%; Score 515; DB 11; Length 145;
Best Local Similarity 68.2%; Pred. No. 1.3e-48;
Matches 88; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

QY 51 ALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSL 110
Db 2 AVGNATGRFAYTPAMESLCGYVHKSQNRSEEFLLAGLQDGLHITTCFVAPWNSLSL 61

QY 111 AORRGFTKTYTGCEECTVFPCLSPCKLQSGTHCLTDLQSGSEKGFQSRHLACLPRE 170
Db 62 AQQKAFVTKYSAGCGVCTVFPCLSPCKLQSGTHCLTDLQSGSEKGFQSRHLACLPRN 121

QY 171 PGLCTWQSL 179
Db 122 PDLCTWQYL 130

RESULT 4
Q925Q6
ID Q925Q6 PRELIMINARY; PRT; 194 AA.
AC Q925Q6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-2 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Ko K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;
RA "Expression of metalloproteinase-2 (gelatinase A) and tissue inhibitor
RT of metalloproteinase-2 (TIMP-2) from hamster tracheal goblet cells: a
RT possible role in upper airway inflammation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260255; AAK51636.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 194
SQ SEQUENCE 194 AA; 21763 MW; 1C5D10A3D38A8941 CRC64;

Query Match 36.5%; Score 368.5; DB 11; Length 194;
Best Local Similarity 40.8%; Pred. No. 2.2e-32;
Matches 75; Conservative 27; Mismatches 67; Indels 15; Gaps 6;

QY 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPVNO--TTLVQ-----RYEIKMTKMYKGFQALG 53
Db 1 CSCSPVHQQAFCNADVVIRAKVSEKVDGNDIYGNPVKRIQYIEIKQIMFK-----G 55

QY 54 DAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGLQDGLHITTCFVAPWNSLSLAQ 112
Db 56 PDKDIEFTYTPAMSCMG-VSLDVGKKEYLIAGKAGDGNHITLCLDFIVPMDTLSTTQ 114

QY 113 RRGFTKTYTGCEECTVFPCLSPCKLQSGTHCLTDLQSGSEKGFQSRHLACLPREPG 172
Db 115 KSLNHHRYQMGCECKITRCMPICYISSPDECLMDWMTVEKSIHQHQAFFACIKRSDG 173

QY 173 LCTW 176
Db 174 SCW 177

RESULT 5
Q9TTB7
ID Q9TTB7 PRELIMINARY; PRT; 152 AA.
AC Q9TTB7;
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DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Metalloproteinase inhibitor 3 (TIMP-3) (Tissue inhibitor of
 metalloproteinase-3) (Fragment).
 GN TIMP-3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs."
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 AND IRREVERSIBLY INACTIVATES THEM, MAY FORM PART OF A TISSUE-
 SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 DB EMBL: AF156031; AAF17356.1; --
 DR HSSP: P16035; 1BR9.
 DR InterPro: IPR001820; TIMP.
 DR Pfam: PF00965; TIMP; 1.
 DR SMART: SM00206; TIMP; 1.
 KW Metalloproteinase inhibitor.
 FT NON TER 1 1
 FT DISULFID 2 109 BY SIMILARITY.
 FT DISULFID 116 121 BY SIMILARITY.
 FT DISULFID 129 150 BY SIMILARITY.
 FT NON TER 152
 SQ SEQUENCE 152 AA; 17736 MW; 4050E5F5FC5B85E7 CRC64;
 RESULT 6
 O9TTB6 PRELIMINARY; PRT; 170 AA.
 ID O9TTB6;
 AC O9TTB6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Metalloproteinase inhibitor 4 (TIMP-4) (Tissue inhibitor of
 metalloproteinase-4) (Fragment).
 GN TIMP-4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs."
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 AND IRREVERSIBLY INACTIVATES THEM.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.

DR EMBL: AF156032; AAF17357.1; --
 DR HSSP: P16035; 2TMP.
 DR InterPro: IPR001820; TIMP.
 DR Pfam: PF00965; TIMP; 1.
 DR SMART: SM00206; TIMP; 1.
 KW Metalloproteinase inhibitor.
 FT NON TER 1
 FT DISULFID 107 154 BY SIMILARITY.
 FT DISULFID 112 117 BY SIMILARITY.
 FT DISULFID 125 146 BY SIMILARITY.
 FT NON TER 170
 SQ SEQUENCE 170 AA; 19831 MW; 29B6412F2D42817D CRC64;
 Query Match 27.9%; Score 282; DB 6; Length 170;
 Best Local Similarity 36.2%; Pred. No. 5,8e-23;
 Matches 51; Conservative 30; Mismatches 54; Indels 6; Gaps 4;
 OY 37 REIKMTKMYKGFQALGDADIRFYVTPAMESVCGYFHRSHNRSEFLIAGK-LDGLLH 95
 DB 21 REIKQIKMFKGFEXI---SDIYIYTPFDSILCC-VKLETSQKQYLITGLSDGKVF 76
 OY 96 ITTCSFVAPWNSLSAQRGFTKTYTVCCECTVFPCLSPCKLQSGTHCLMTDQLQSS 155
 DB 77 IHLGVIEPWNLSFLQRESLNHYHLNC-GQITTCYVVPCTISAPNECIATWDLLEOK 135
 OY 156 EKGQSRHLACLPREPGLCTW 176
 DB 136 LVGYQAQHYVCKMKAHDGTCW 156
 RESULT 7
 O9TTB8 PRELIMINARY; PRT; 138 AA.
 ID O9TTB8;
 AC O9TTB8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Metalloproteinase inhibitor 2 (TIMP-2) (Tissue inhibitor of
 metalloproteinase-2) (Fragment).
 GN TIMP-2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs."
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 AND IRREVERSIBLY INACTIVATES THEM.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
 DISULFIDE BONDS.
 CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 DB EMBL: AF156030; AAF17355.1; --
 DR HSSP: P16035; 1BR9.
 DR InterPro: IPR001820; TIMP.
 DR Pfam: PF00965; TIMP; 1.
 DR SMART: SM00206; TIMP; 1.
 KW Metalloproteinase inhibitor.
 FT NON TER 1
 FT DISULFID 117 122 BY SIMILARITY.
 FT NON TER 138
 SQ SEQUENCE 138 AA; 15596 MW; F43F13651F45C348 CRC64;
 Query Match 24.4%; Score 246.5; DB 6; Length 138;
 Best Local Similarity 39.7%; Pred. No. 3,6e-19;
 Matches 56; Conservative 19; Mismatches 51; Indels 15; Gaps 6;
 OY 17 LVIRAKFVGTPEVNO-TTLVYQ-----RYEIKMTKMYKGFQALGDADIRFYVTPAMESV 69
 DB 1 VVIRAKAVSEKVDGNDIYGNPIRIQYIKQIMFK-----GPKDIEFYTAPSSAV 55

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QY 70 CGYFHRSHNRSEFLIAGKLO-DGLLHITTCFVAPWNSLSLAQRGFTKTYTVCBECT 128
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 56 CG-VSLDIGGKEYIAGAGGKXMTLCLDFIVPMDTLSTQKSLNHRVQMGCECK 113
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 129 VFPCLSIPOKLGSTHCLMTD 149
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 114 ITRCPMIPCIYSSPDECLMWD 134
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

RESULT 8
Q95KL7 PRELIMINARY; PRT; 126 AA.
AC Q95KL7.
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-3 (Fragment).
GN TIMP-3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]_TaxID=9544;
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ji S., Wang Y., Li H., Ji W., Piao Y.;
RT "Cloning and characterization of tissue inhibitor of matrix
RT metalloproteinase-3 (TIMP-3) cDNA from Macaca mulatta.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366399; AAK53706.1; -
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 126 AA; 14690 MW; 2F162249A7D2615E CRC64;

Query Match 23.0%; Score 232.5; DB 6; Length 126;
Best Local Similarity 37.6%; Pred. No. 1.1e-17;
Matches 50; Conservative 27; Mismatches 45; Indels 11; Gaps 5;

QY 12 FCNSDLVIRAKVCGTPEVQNQ---TTLQRYEIKMTKMYKGFOALGDAADIRFVYTPAMES 68
|||||:|||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 1 FCNSDIVIRAKVVGKKLVKEGPFGLV--YTIKQMKMYRGFTKM--PHVQVIHTEASES 55
|||||:|||||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

QY 69 VCGYFHRSHNRSEFLIAGKLODGLLHITTCFVAPWNSLSLAQRGFTKTYTVCBECT 128
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 56 LCGL--KLEVNKYQYLLTGRVVDGKMYTCLCNFVERWDQLTSLQRKGLNRYHLGC-NCK 112
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

QY 129 VFPCLSIPOKLGSTHCLMTD 141
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 113 IKSCVYLPCEFTS 125
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

RESULT 9
Q95KL8 PRELIMINARY; PRT; 97 AA.
AC Q95KL8.
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-2 (Fragment).
GN TIMP-2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]_TaxID=9544;
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ji S., Wang Y., Li H., Ji W., Piao Y.;
```

```
RT "Cloning and characterization of tissue inhibitor of matrix
RT metalloproteinase-2 (TIMP-2) cDNA from Macaca mulatta.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366398; AAK53705.1; -
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 11224 MW; 1AA2387A2802533C CRC64;

Query Match 18.7%; Score 188.5; DB 6; Length 97;
Best Local Similarity 38.3%; Pred. No. 5.5e-13;
Matches 31; Conservative 14; Mismatches 35; Indels 1; Gaps 1;

QY 96 ITTCSFVAPWNSLSLAQRGFTKTYTVCBECTVFPCLSIPOKLGSTHCLMTDQLLOGS 155
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 1 ITLCDFIVPMDTLSTQKSLNHRVQMGCECKITRCFMPICYSPPDECLMMDWVTEKN 59
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

QY 156 EKGFSQSRHLACLPREPGLCTW 176
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 60 INGHQAKFFACIKRSDGSCAW 80
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

RESULT 10
Q9GPJ2 PRELIMINARY; PRT; 221 AA.
AC Q9GPJ2.
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Tissue inhibitor of metalloproteinase TIMP.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Metazoa; Mollusca; Bivalvia; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]_TaxID=29159;
RP SEQUENCE FROM N.A.
RC MEDLINE=21329024; PubMed=11434928;
RA Montagnani C., Le Roux F., Berthe F., Escoubas J.M.;
RT "Cg-TIMP, an inducible tissue inhibitor of metalloproteinase from the
RT Pacific oyster Crassostrea gigas with a potential role in wound
RT healing and defense mechanisms.";
RL FEBS Lett. 500:64-70(2001).
DR EMBL; AF321279; AAC42824.1; -
DR HSPP; P16035; IBR9.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR SWART; SM00206; TIMP; 1.
SQ SEQUENCE 221 AA; 25332 MW; AA53F67EB137A06A CRC64;

Query Match 18.0%; Score 181.5; DB 5; Length 221;
Best Local Similarity 26.8%; Pred. No. 8.4e-12;
Matches 53; Conservative 30; Mismatches 84; Indels 31; Gaps 8;

QY 1 CTCVPPHPOTAFCSNLDLIRAKFV-----GTP---EVNQTLYQRYEIKMTKMY 46
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 23 CMCDFTHPQNNFCSADFVIRATIVKELKFGDESMGIPFLQKNYVQFKKRD1-----F 77
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

QY 47 KGFOALGDAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLODGLLHITTCFVAPWN 106
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 78 KGSSLLG-SSDTLVIKTSGTPWNCG---EFTLNKEYVISGFVSDGEFFTNCCQNPYL 133
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

QY 107 SLSLAQRGFTKTYTVCBECTVFPCC---LSIPCKLQSGTHCLMTDQLLOGSEKGFQSR 162
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 134 TLEPHQRGIRYMYEQGC-NCTIHCRCGNCDFPQSLNPQDTCIWPGSY---NTNDCYAK 189
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

QY 163 HLACLPREPGICTWQSLR 180
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
DB 190 YGFCPLDIFGVYWKQNR 207
|| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|

RESULT 11
Q61720 PRELIMINARY; PRT; 38 AA.
ID Q61720
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```
AC Q61720;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Messenger RNA fragment for mouse interferon beta (Type 1) coding for
DE the c-terminal part (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82247191; PubMed=6179042;
RA Skup D., Windass J.D., Sor F.S., George H., Williams B.R.,
RA Fukushima H., De Maeyer-Guignard J., De Maeyer E.;
RT "Molecular cloning of partial cDNA copies of two distinct mouse IFN-
RT beta mRNAs."
RL Nucleic Acids Res. 10:3069-3084(1982).
DR EMBL; V00755; CAA24132.1; -
DR HSSP; P01033; IUBA.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
FT NON_TER 1
SQ SEQUENCE 38 AA; 4390 MW; 7837C934C664BC7F CRC64;

Query Match 14.8%; Score 149.5; DB 11; Length 38;
Best Local Similarity 75.0%; Pred. No. 3.5e-09;
Matches 27; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Oy 144 HCLMTDQLQSGSEKGFQSHLACLPREPGLCTWQSL 179
Db 1 HCLMTDQVLVQSE-DYQSRHFACLPRLGLCTWRSI 35

RESULT 12
Q80U22 PRELIMINARY; PRT; 97 AA.
AC Q80U22;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tissue inhibitor of metalloproteinase 2 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105266; PubMed=7806596;
RA Leco K., Jung J.-C., Fini M., Edwards D.R.;
RT "Role of Matrix Metalloproteinase in Metamorphic Tadpole Tail
RT Resorption."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037944; AAL01592.1; -
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SMO0206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
DR PROSITE; PS00288; TIMP; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 10646 MW; DDE1F6CD749E5803 CRC64;

Query Match 12.8%; Score 129.5; DB 13; Length 97;
Best Local Similarity 49.1%; Pred. No. 1.6e-06;
Matches 27; Conservative 8; Mismatches 13; Indels 7; Gaps 2;

Oy 1 CTCVPHPTAFGNSDLVIRAKFVGTPV-NTTLYO-----RYEIKMTKMYKG 48
Db 38 CSCSPVHPQATFNSDLVIRAKAIGTKVDNGNDVYGNFIKTIQYFIKTIKMFKG 92

RESULT 13
Q90UW9 PRELIMINARY; PRT; 280 AA.
AC Q962H0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
```

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ID Q90UW9 PRELIMINARY; PRT; 25 AA.
AC Q90UW9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ENDOPEPTIDOLYSIS protein-II (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96094433; PubMed=8530636;
RA Sharpe-Timms K.L., Penney L.L., Zimmer R.L., Wright J.A., Zhang Y.,
RA Surewicz K.;
RT "Partial purification and amino acid sequence analysis of
RT endopeptidolysis protein-II (ENDO-II) reveals homology with tissue
RT inhibitor of metalloproteinases-1 (TIMP-1).";
RL J. Clin. Endocrinol. Metab. 80:3784-3787(1995).
DR HSSP; P01033; IUBA.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
FT PROSITE; PS00288; TIMP; 1.
SQ SEQUENCE 25 AA; 2698 MW; 35129B2B74C1FPAF CRC64;

Query Match 12.3%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e-06;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CTCVPHPTAFGNSDLVIRAKFVG 25
Db 1 CSCAPTHPTAFGNSDLVIRAKFVG 25

RESULT 14
Q90V13 PRELIMINARY; PRT; 25 AA.
AC Q90V13;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Collagenase inhibitor MS-31 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105266; PubMed=7806596;
RA Rosenthal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,
RA Folkman J.;
RT "Purification and characterization of two collagenase inhibitors from
RT mouse sarcoma 180 conditioned medium.";
RL J. Cell. Biochem. 56:97-105(1994).
DR HSSP; P01033; IUBA.
DR InterPro: IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
SQ SEQUENCE 25 AA; 2678 MW; 923226E82C1901FD CRC64;

Query Match 12.3%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3e-06;
Matches 21; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TCVPHPTAFGNSDLVIRAKFVG 26
Db 1 SCAPVPTAFGNSDLVIRAKFVG 25

RESULT 15
Q962H0 PRELIMINARY; PRT; 280 AA.
AC Q962H0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
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DT 01-DEC-2001 (TRENBLrel. 19; Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21; Last annotation update)
DE Tensilin.
OS Cucumaria frondosa.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Holothuroidea; Dendrochirotacea; Dendrochirotida; Cucumariidae;
OC Cucumaria.
OX NCBI_TaxID=36326;
RN [1]
RP SEQUENCE FROM N.A.
RA Tipper J.P., Trotter J.A.;
RT "Cloning of tensilin cDNA: the stiffening factor in sea cucumber inner
RT dermis."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033934; AAK61535.1; -
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
SQ SEQUENCE 280 AA; 31528 MW; 00A6273DF52DA241 CRC64;

Query Match 10.6%; Score 106.5; DB 5; Length 280;
Best Local Similarity 20.8%; Pred. NO. 0.0019;
Matches 44; Conservative 34; Mismatches 75; Indels 59; Gaps 12;

QY 3 CVPHPQTAFGNSDLVIRAKFV-----GTPEVNTLYQRYEIKWTKMYKGFQALGD 54
DB 25 CSVKHPQHHCDAFTVMKVITIDVLDROGGDKLIN-----AEINRSWKGPS 72

QY 55 AADIRFVYTPAMESVCGYFHRSHNRSEBFLIAG---KLQDG---LLHITTCFVAPMNSL 108
DB 73 SCDFOF-YAPS--SFCG---ATFDSGTYVVVTGKETS DGRYWLH-GSCDYMIKWDDM 125

QY 109 SLAQRGFTKTYTGCECTVPPCLS-----IPCKLQSGTHC-----LWTD 149
DB 126 SDQKAGFGGKYKARCQIAESLTAASVKVEDIAANDYPLATTYWTPTGCVYNPLMTR 185

QY 150 QLLQSEKG-----FQSRHLACLREPGLCTW 176
DB 186 QFV--GRKGSSVVDCEVDYGLCKPNEADKCQW 215

Search completed: December 17, 2002, 15:08:09
Job time : 35.6276 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 8.4069 Seconds
(without alignments)
370.985 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579

Sequence: 1 CTCVPHPHQTAFCNSDLVIR.....GKLQDGLHTTCSFVAPWN 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequences: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/PTOS.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backlist1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	579	100.0	184	4	US-09-452-817-1
3	579	100.0	207	1	US-08-588-163-5
4	579	100.0	207	2	US-09-111-070-5
5	579	100.0	207	4	US-08-849-764C-5
6	579	100.0	207	4	US-09-262-087-5
7	579	100.0	207	4	US-08-463-261B-11
8	234	40.4	220	1	US-08-588-163-3
9	234	39.0	218	4	US-09-111-070-3
10	226	39.0	218	4	US-08-849-764C-3
11	226	39.0	218	4	US-09-262-087-3
12	226	39.0	218	4	US-08-463-261B-9
13	215	37.1	211	1	US-08-588-163-4
14	215	37.1	211	2	US-09-111-070-4
15	209.5	36.2	210	4	US-08-849-764C-4
16	209.5	36.2	210	4	US-09-262-087-4
17	209.5	36.2	210	4	US-08-463-261B-10
18	201.5	34.8	224	1	US-08-588-163-2
19	201.5	34.8	224	4	US-09-111-070-2
20	201.5	34.8	224	4	US-08-849-764C-2
21	201.5	34.8	224	4	US-09-262-087-2
22	201.5	34.8	224	4	US-08-463-261B-2
23	201.5	34.8	224	5	PCT-US94-14498A-2
24	124	21.4	25	2	US-08-474-696A-2
25	105	18.1	22	2	US-08-474-696A-5
26	105	18.1	22	2	US-08-474-696A-6
27	105	18.1	25	2	US-08-474-696A-4

28	77	13.3	16	2	US-08-480-190-134	Sequence 134, App
29	77	13.3	16	2	PCT-US93-07545-134	Sequence 134, App
30	77	13.3	16	5	PCT-US93-07545-134	Sequence 134, App
31	72	12.4	15	2	US-08-480-190-135	Sequence 247, App
32	72	12.4	15	2	US-08-480-190-247	Sequence 247, App
33	72	12.4	15	2	US-08-488-379-135	Sequence 135, App
34	72	12.4	15	2	US-08-488-379-247	Sequence 247, App
35	72	12.4	15	5	PCT-US93-07545-135	Sequence 135, App
36	72	12.4	15	5	PCT-US93-07545-247	Sequence 247, App
37	65	11.2	406	4	US-09-134-001C-5330	Sequence 5330, App
38	64	11.1	1079	3	US-09-136-652-2	Sequence 2, App1
39	61	10.5	1809	3	US-09-012-515A-12	Sequence 12, App1
40	61	10.5	1809	4	US-08-360-144A-12	Sequence 12, App1
41	61	10.5	1809	4	US-09-012-504A-12	Sequence 12, App1
42	61	10.5	2549	4	US-08-471-112A-3	Sequence 3, App1
43	61	10.5	2549	5	PCT-US95-06722-12	Sequence 12, App1
44	60	10.4	383	4	US-09-134-001C-3701	Sequence 3701, App
45	59.5	10.3	1882	4	US-09-369-364A-13	Sequence 13, App1

ALIGNMENTS

RESULT 1
US-09-452-817-2
; Sequence 2, Application US/09452817
; Patent No. 6342374

GENERAL INFORMATION:

APPLICANT: Carmichael, David F

APPLICANT: Anderson, David C

APPLICANT: Stricklin, George P

APPLICANT: Weigus, Howard G

TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System

TITLE OF INVENTION: For Using Same And Recombinant DNA Method For

FILE REFERENCE: Serial No. 6342374 09/452,817

CURRENT FILING DATE: 2001-06-22

PRIOR FILING DATE: 08/474,553

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/050,739

PRIOR FILING DATE: 1993-04-21

PRIOR APPLICATION NUMBER: 07/853,018

PRIOR FILING DATE: 1992-03-18

PRIOR APPLICATION NUMBER: 07/517,475

PRIOR FILING DATE: 1990-05-01

PRIOR APPLICATION NUMBER: 07/320,923

PRIOR FILING DATE: 1989-03-08

PRIOR APPLICATION NUMBER: 06/784,319

PRIOR FILING DATE: 1985-10-04

PRIOR APPLICATION NUMBER: 06/699,181

PRIOR FILING DATE: 1985-02-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 106

TYPE: PRT

ORGANISM: Homo sapiens

US-09-452-817-2

Query Match 100.0%; Score 579; DB 4; Length 106;

Best Local Similarity 100.0%; Pred. No. 3 4e-71;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	CTCVPHPHQTAFCNSDLVIRAKVGTPEVNOITLYQRYEIKWTXMYKGFQALGDAADIRF	60
QY	61	VYTPMESVCGYFHRSHNRSEFLIAGKLODGLHTTCSFVAPWN	106
DB	61	VYTPMESVCGYFHRSHNRSEFLIAGKLODGLHTTCSFVAPWN	106

TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: METALLOPROTEINASES
CLONE: TIMP-1
US-09-111-070-5

Query Match 100.0%; Score 579; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.7e-71;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60
24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPVAPWN 106
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPVAPWN 129

RESULT 5
US-08-849-764C-5
Sequence 5, Application US/08849764C
Patent No. 6300310

GENERAL INFORMATION:

APPLICANT: GREENE, JOHN M
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,764C
FILING DATE: 19-Sep-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MICHELE M. WALES
REGISTRATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: PFI48US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-849-764C-5

Query Match 100.0%; Score 579; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.7e-71;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPVAPWN 106
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPVAPWN 129

RESULT 6
US-09-262-087-5
Sequence 5, Application US/09262087
Patent No. 6391853

GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,087
FILING DATE: 04-MAR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,261
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14498
FILING DATE: 13-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PFI48PID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-262-087-5

Query Match 100.0%; Score 579; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.7e-71;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPVAPWN 106
DB 84 VYTPAMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPVAPWN 129

RESULT 7

US-08-463-261B-11
; Sequence 11, Application US/08463261B
; Patent No. 6448042
; GENERAL INFORMATION:
; APPLICANT: John M. Greene and Craig A. Rosen
; TITLE OF INVENTION: Human Tissue Inhibitor of Metalloproteinase-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,261B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14498
; FILING DATE: 13-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PFI48P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 301-610-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-463-261B-11
Query Match 100.0%; Score 579; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.7e-71;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVPPHPQTAFCSNLDLIRAKFVGTPEVNTTLQRYEIKTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDLIRAKFVGTPEVNTTLQRYEIKTKMYKGFQALGDAADIRF 83
Qy 61 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWN 106
Db 84 VYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWN 129
RESULT 8
US-08-588-163-3
; Sequence 3, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,163
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-2
US-08-588-163-3
Query Match 40.4%; Score 234; DB 1; Length 220;
Best Local Similarity 44.7%; Pred. No. 9e-24;
Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;
Qy 1 CTCVPPHPQTAFCSNLDLIRAKFVGTPEVNTTLQY-----RYEIKTKMYKGFQALG 53
Db 27 CSCSPVHPQAFCSNLDLIRAKFVGTPEVNTTLQY-----RYEIKTKMYKGFQALG 81
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLDGLLHITTCFVAPWN 106
Db 82 PEKIDIEFIYTPSSAVCG-VSLDVGGKKEYLIAGKAGDGKWHITLCDFIIVPWD 134
RESULT 9
US-09-111-070-3
; Sequence 3, Application US/09111070
; Patent No. 5914392
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: METALLOPROTEINASES
CLONE: TIMP-2
UN-09-111-070-3
Query Match 40.4%; Score 234; DB 2; Length 220;
Best Local Similarity 44.7%; Pred. No. 9e-24; Mismatches 34; Indels 14; Gaps 5;
Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;
Qy 1 CTCVPHPQTAFNSDLVIRAFVGTPEVNO-TTLYQ-----RVEIKMTKMYKGFQALG 53
Db 27 CSCSPVHPQOAFNCADVIRAKAVSEKVDGNDIYGNPIKRIYIYIKI-KMFK-----G 81
Qy 54 DAADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCSEFVAPWN 106
Db 82 PEKDIEFIYTPASSAVCG-VSLDVGSKKEYLLIAGKAKEGDGKXKHITLDFPIVPM 134

RESULT 10
US-08-849-764C-3
Sequence 3, Application US/08849764C
Patent No. 6300310
GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
ROSEN, CRAIG
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,764C
FILING DATE: 19-Sep-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MICHELE M. WALES
REGISTRATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: PF148US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-849-764C-3
Query Match 39.0%; Score 226; DB 4; Length 218;
Best Local Similarity 44.2%; Pred. No. 1.1e-22;
Matches 50; Conservative 16; Mismatches 33; Indels 14; Gaps 5;
Qy 1 CTCVPHPQTAFNSDLVIRAFVGTPEVNO-----TTLYQRYEIKMTKMYKGFQALGD 54
Db 27 CSCSPVHPQOAFNCADVIRAKAVSEKVDGNDIYGNPIKRIYIYIKI-KMFK-----GP 80
Qy 55 AADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCSEFVAPWN 106
Db 81 EKDIIEFIYTPASSAVCG-VSLDVGSKKEYLLIAGKAKEGDGKXKHITLDFPIVPM 132

RESULT 11
US-09-262-087-3
Sequence 3, Application US/09262087
Patent No. 6391853
GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
ROSEN, CRAIG
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,087
FILING DATE: 04-MAR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,261
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14498
FILING DATE: 13-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF148PID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-262-087-3
Query Match 39.0%; Score 226; DB 4; Length 218;
Best Local Similarity 44.2%; Pred. No. 1.1e-22;
Matches 50; Conservative 16; Mismatches 33; Indels 14; Gaps 5;
Qy 1 CTCVPHPQTAFNSDLVIRAFVGTPEVNO-----TTLYQRYEIKMTKMYKGFQALGD 54
Db 27 CSCSPVHPQOAFNCADVIRAKAVSEKVDGNDIYGNPIKRIYIYIKI-KMFK-----GP 80
Qy 55 AADIRFVYTPAMESVCGYFHRSHNRSEFLIAGKLQ-DGLLHITTCSEFVAPWN 106


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:      FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/568,163
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Luther, Barbara J.
: REGISTRATION NUMBER: 33,954
: REFERENCE/DOCKET NUMBER: PF-0053
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-852-0195
:
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 211 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: polypeptide
: IMMEDIATE SOURCE:
: LIBRARY: METALLOPROTEINASES
: CLONE: T1MP-3
:
: US-09-111-070-4
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Best Local Similarity	41.3%	Pred. No. 3.3e-21;	
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Qy 1 CTCVPRHPQIAFNSLSVIRAFVGTPEVNO---TLYVQRFEIIMTGYGFPALDDAD 57
Db 24 CTCSPHPQAFNSDVIIRAKVVGKKLVKSGPFTLV--TLYQMGMVYGFIRM---PH 78

Qy 58 IRVVPRAMESVCGYFHRSHNSSEFLAGLQGLAHITTCSEVAPWN 106
Db 79 VQYIIRBASESLQGL--KLEVNVKYLILGRVYDKMTGLCNVVERMD 125

RESULT 15
 US-08-849-764C-4
 : Sequence 4, Application US/08849764C
 : Patent No. 6300310
 :
 : GENERAL INFORMATION:
 : APPLICANT: GREENE, JOHN M
 : ROSEN, CRAIG
 :
 : TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
 : METALLOPROTEINASE-4
 :
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 : STREET: 9410 KEY WEST AVENUE
 : CITY: ROCKVILLE
 : STATE: MD
 : COUNTRY: USA
 : ZIP: 20850
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/849,764C
 : FILING DATE: 19-Sep-1997
 : CLASSIFICATION: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: MICHELE M. WALES
 : REGISTRATION NUMBER: 43,975
 : REFERENCE/DOCKET NUMBER: PF148US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 301-309-8504
 : TELEFAX: 301-309-8439
 :
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:

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?      LENGTH: 210 amino acids
?      TYPE: amino acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
?      SS-08-849-764C-4

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Query Match	36.2%	Score 209.5	DB 4	Length 210
Best Local Similarity	41.3%	Pred. No. 1	8e-20	
Matches	45	Conservative	18	Mismatches 35
				Indels 11
				Gaps 4

Qy 1 CTCVPHPTACNSDLVIRAKVGTSPVNO---TTLQCYEIMTMYGFOALDDAD 57
Db 24 CTCSPHQDARCNSDLVIRAKVCKLVRKSGRPTLV--YTIKQMYMGTFKPMYH-- 79

Qy 58 IRVVYPRMSEVCGYFHSHNRSEEFILAGLQDGLLHTTSCSVAPWYN 106
Db 80 --YTHHSEASESLGL--KLEVNKYQYLLTGLGVYDGKMTGLCNVERWD 124

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Job time : 9.4069 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
594.503 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579
Sequence: 1 CTCVPHPHQTAFCNSDLVIR.....GKLDGLHTTCSFVAPWN 106

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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%
Maximum March 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	127	23	AAU99886
2	579	100.0	128	23	AAU99887
3	579	100.0	184	23	AAU99875
4	579	100.0	204	23	ABP42206
5	579	100.0	207	7	ABP60786
6	579	100.0	207	7	ABP60275
7	579	100.0	207	7	ABP60592
8	579	100.0	207	18	AAW30309
9	579	100.0	207	20	AAV08933
10	579	100.0	207	21	AAI19073

11	579	100.0	207	22	AAW33377
12	579	100.0	207	22	AAW39171
13	579	100.0	522	23	AAU99883
14	579	100.0	522	23	AAU99885
15	579	100.0	580	23	AAU99882
16	579	100.0	580	23	AAU99889
17	576	99.5	207	7	AAW60593
18	565	97.6	207	16	AAW65005
19	558	96.4	183	21	AAW44149
20	508	87.7	207	16	AAW65003
21	507	87.6	206	16	AAW65006
22	494	85.3	207	16	AAW65004
23	491	84.8	162	23	ABP42434
24	484	83.6	212	23	ABP42381
25	458	79.1	205	16	AAW65007
26	428.5	74.0	207	16	AAW65008
27	239.5	41.4	192	11	AAW06895
28	236.5	40.8	193	23	AAW60277
29	236	40.8	47	7	ABP60276
30	235	40.6	194	23	AAW60276
31	234	40.4	194	21	ABW08904
32	234	40.4	220	11	AAW07955
33	234	40.4	220	15	AAW62769
34	234	40.4	220	16	AAW65009
35	234	40.4	220	19	AAW48253
36	234	40.4	220	20	AAW08931
37	234	40.4	220	21	AAW19074
38	234	40.4	220	21	AAW15137
39	234	40.4	237	23	AAW60278
40	233	40.2	194	23	AAW67031
41	233	40.2	220	23	AAW67031
42	227	39.2	220	11	AAW62768
43	227	39.2	220	15	AAW48256
44	227	39.2	220	19	AAW48256
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ALIGNMENTS

RESULT 1	AAU99886	standard; Protein; 127 AA.
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AC	AAU99886;	
XX		
DT	07-OCT-2002	(first entry)
XX		
DE	Human TIMP 1-127 protein.	
XX		
KW	TIMP 1-127; Alzheimer's disease; tumour angiogenesis;	Human polypeptide,
KW	malaria; emphysema; asthma; chronic obstructive pulmonary disease;	Human secreted pro
KW	cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;	Human secreted pro
KW	human immunodeficiency virus; atopic dermatitis; muscular dystrophy;	Human secreted pro
KW	herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;	Human secreted pro
KW	tumour metastasis; osteoporosis; Paget's disease; scleroderma;	Human secreted pro
KW	glomerulonephritis; hypertension.	Human secreted pro
OS	Homo sapiens.	Human secreted pro
XX		
PN	WO200250287-A2.	Human secreted pro
XX		
PD	27-JUN-2002.	Human secreted pro
XX		
PF	18-DEC-2001; 2001WO-US49256.	Human secreted pro
XX		
PR	18-DEC-2000; 2000US-256699P.	Human secreted pro
XX		
PR	20-NOV-2001; 2001US-331966P.	Human secreted pro
XX		
PA	(ARRI-) ARRIYA PHARM INC.	Human secreted pro
XX		
PI	Barr PJ, Gibson HL, Pemberton P;	Human secreted pro
XX		

XX 18-DEC-2001; 2001WO-US49256.
XX
XX 18-DEC-2000; 2000US-256699P.
XX 20-NOV-2001; 2001US-331966P.
XX
XX (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI; 2002-500631/53.
XX N-PSDB; ABK88017.
XX
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease
XX inhibitor -
XX
XX Disclosure; Page 37; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally
XX active portion. The fusion proteins of the invention may act as an
XX inhibitor of protease activity. The fusion protein of the invention
XX is useful for inhibiting protease activity associated with a disorder
XX such as emphysema, asthma, chronic obstructive pulmonary disease,
XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
XX for treating an individual suffering from or at risk for a disease or
XX disorder involving unwanted protease activity. The proteins are useful
XX for treating dermatological diseases such as atopic dermatitis, eczema
XX and psoriasis, inflammatory responses to viral infection, and for
XX treating herpes infection, corneal or epidermal ulceration, chronic
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
XX tumour metastasis and tumour angiogenesis, gastric ulceration,
XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
XX bacterial infection, Alzheimer's disease, hypertension and muscular
XX dystrophy. The present sequence represents the human tissue inhibitor
XX of metalloproteases used to create the fusion protein of the invention.
XX
XX Sequence 184 AA:
XX
XX Query Match 100.0%; Score 579; DB 23; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 9,2e-65;
XX Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60
XX 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60
XX
XX 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 106
XX 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 106
XX
XX 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 106
XX 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 106
XX
XX RESULT 4
XX ABP42206
XX ID ABP42206 standard; Protein; 204 AA.
XX
XX AC ABP42206;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HCOG079, SEQ ID NO:3338.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX Human; ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX Homo sapiens.
XX
XX WO20020677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US18569.
XX
XX 07-JUN-2000; 2000US-209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX N-PSDB; ABQ55283.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases -
XX
XX Claim 11; SEQ ID No 3338; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the
XX identification of individuals and in forensic analysis, and the
XX polypeptides may be used as food additives or to prepare antibodies
XX useful in disease diagnosis, drug targeting and phenotyping. The present
XX sequence represents a human ovarian antigen of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 204 AA:
XX
XX Query Match 100.0%; Score 579; DB 23; Length 204;
XX Best Local Similarity 100.0%; Pred. No. 1e-64;
XX Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 60
XX 22 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNQTLTYQRYEIKMTKMYKGFQALGDAADIRF 81
XX
XX 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 106
XX 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 106
XX
XX 82 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 127
XX 82 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSPFAPNN 127
XX
XX RESULT 5

AAP60786
ID AAP60786 standard; Protein; 207 AA.

XX

AC AAP60786;

XX

DT 08-AUG-1991 (first entry)

XX

DE Sequence of tissue inhibitor of metalloproteinase (TIMP).

XX

KW Connective tissue; extracellular matrix.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

FT Protein 24..207

FT Modified-site 53..55

FT /label= potential N-glycosylation site

FT Modified-site 101..103

FT /label= as above

XX

PN GB2169295-A.

XX

PD 09-JUL-1986.

XX

PF 06-JAN-1986; 85GB-0000199.

XX

PR 01-NOV-1985; 85GB-0026951.

XX

PR 07-JAN-1985; 85GB-0000341.

XX

PR 06-JAN-1986; 85GB-0000199.

XX

PR 07-JAN-1985; 85GB-0500341.

XX

PR 05-OCT-1983; 83BE-0897924.

XX

PA (CELL-) CELLTECH LTD.

XX

PI Harris TJR, Reynolds JJ, Docherty AJP, Murphy G;

XX

DR WPI; 1986-177873/28.

XX

DR N-PSDB; AAN60538.

XX

XX Prodn. of metallo-proteinase inhibitors - by recombinant DNA

FT techniques

XX

PS Disclosure; Fig 3; 16pp; English.

XX

CC A gene with residues 64-684 of AAN60538 is claimed. AAN60538 was

CC isolated from human a foetal diploid lung cells (ATCC CCL153) cDNA

CC library using AAN60539.

XX

SQ Sequence 207 AA;

XX

Query Match

Best Local Similarity 100.0%; Score 579; DB 7; Length 207;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60

Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106

Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

XX

RESULT 6

AAP60275

ID AAP60275 standard; Protein; 207 AA.

XX

AC AAP60275;

XX

DT 03-OCT-2002 (updated)

XX

DT 08-AUG-1991 (first entry)

XX

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Sequence of human natural inhibitor of collagenases (NIC).

XX

KW Metallo-proteinase inhibitor; wound healing; emphysema;

XX

KW rheumatoid arthritis therapy; ulceration; tumour metastasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

FT Protein 24..207

FT /note= "claimed"

FT Modified-site 53..55

FT /note= "potential glycosylation site"

FT Modified-site 101..103

FT /note= "potential glycosylation site"

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FH

XX Homo sapiens.
OS W08602100-A.
XX PD 10-APR-1986.
XX PF 01-OCT-1985; 85WO-5001900.
XX PR 01-OCT-1984; 84US-0656590.
XX (SANO) SANDOZ LTD.
PA (REGC) REGENTS OF UNIV OF CALIFO.
PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;
XX WPI; 1986-106663/16.
DR N-PSDB; AAN60494.
XX
XX Vectors contg. gene for protein having erythroid potentiating
PT activity - used for producing protein to stimulate growth and
XX formation of erythroid cells
XX
XX Disclosure; Fig 4; 59pp; English.
XX
XX The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)
CC and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a
CC biological activity of at least about 1,000,000 units per mg of
CC protein and has an apparent molecular weight of about 28,000 daltons.
XX
SQ Sequence 207 AA;
Query Match 100.0%; Score 579; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 129
RESULT 8
AAN30309
AAN30309 standard; Protein; 207 AA.
AC AAN30309;
XX
XX 29-JAN-1998 (first entry)
XX
XX Human TIMP-1.
XX
XX TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;
XX cancer progression; TIMP-1.
XX
XX Homo sapiens.
OS
XX JP09235300-A.
XX PD 09-SEP-1997.
XX PF 29-FEB-1996; 96JP-0067484.
XX PR 29-FEB-1996; 96JP-0067484.
XX (FUJY) FUJI PHARM IND CO LTD.
XX WPI; 1997-498341/46.
XX N-PSDB; AAT92631.
XX

PT Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used in
PT diagnosis of TIMP-3 mediated diseases, especially the detection of
PT malignant tumour cells
XX
XX Example 12; Page 33-34; 37pp; Japanese.
XX
XX This sequence represents the human TIMP-1 protein. This sequence was
CC used to test the specificity of the monoclonal antibody (Mab) of the
CC invention. The Mab of the invention reacts specifically with human
CC TIMP-3 (see AAN30308), by specific recognition of the TIMP-3 fragments
CC represented by AAN30305-W30307. The Mab can be used in the study or
CC diagnosis of TIMP-3-mediated diseases, particularly for the detection of
CC malignant tumour cells, or the diagnosis of progressiveness of cancers.
CC They can also be used in establishing an immunoassay for TIMP-3 or in
CC purification of TIMP-3. The transformed cells can be used for producing
CC TIMP-3 or its equivalent proteins on a large scale. The immunoassay
CC method for TIMP-3 the Mabs is simple, highly reproducible and highly
CC sensitive.
XX
SQ Sequence 207 AA;
Query Match 100.0%; Score 579; DB 18; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-64;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 60
DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLDGLHITTCSFVAPWN 129
RESULT 9
AAY08933
AAY08933 standard; Protein; 207 AA.
AC AAY08933;
XX
XX 19-AUG-1999 (first entry)
XX
XX Human TIMP-1 protein.
XX
XX TIMP-4; tissue inhibitor of metalloprotease; human; antibody; diagnosis;
XX treatment; metastasis; neoplastic cell; angiogenesis; tumour; cervical;
XX uterine; pancreatic; colon; intestinal carcinoma; pregnancy; ulcer;
XX osteoarthritis; pulmonary emphysema; periodontal disease; corneal;
XX rheumatoid arthritis; diabetic ulcer; lesion; TIMP-4.
XX
XX Homo sapiens.
OS
XX US5914392-A.
XX PD 22-JUN-1999.
XX PF 07-JUL-1998; 98US-0111070.
XX PR 18-JAN-1996; 96US-0568163.
XX PR 27-JUN-1997; 97US-0884073.
XX PR 07-JUL-1998; 98US-0111070.
XX (INCY-) INCYTE PHARM INC.
XX
XX Hawkins PR, Murry LE;
XX WPI; 1999-384187/32.
XX
XX Anti-tissue inhibitor metalloproteinase antibodies useful for
PT treating and diagnosing cancer
XX
XX Disclosure; Fig 4; 26pp; English.
XX

CC This invention describes a novel method for the production of antibodies
CC specific for the human tissue inhibitors of metalloproteinase 4, TIMP-4.
CC The anti-TIMP-4 antibodies may be used to treat, prevent or diagnose
CC metastasis of neoplastic cells, angiogenesis and growth tumours such as
CC cervical, uterine, pancreatic, colon or intestinal carcinomas, pregnancy,
CC osteoarthritis, pulmonary emphysema, peridontal disease, rheumatoid
CC arthritis, corneal or diabetic ulcers or ulcers and lesions caused by
CC microorganisms. This sequence represents TIMP-4 which is used to
CC describe the method of the invention.

XX SQ Sequence 207 AA;
XX
XX Query Match 100.0%; Score 579; DB 20; Length 207;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-64;
XX Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLVQRYEIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLVQRYEIKMTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWN 106
DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWN 129

RESULT 10
AAB19073
ID AAB19073 standard; protein; 207 AA.
XX
XX AC AAB19073;
XX
XX DT 08-FEB-2001 (first entry)
XX
XX DE Inhibitor of tissue metalloproteinase designated TIMP-1.
XX
XX KW Tissue metalloproteinase inhibitor; TIMP; metalloproteinase; gelatinase;
XX metastasis; cancer.
XX
XX OS Unidentified.

XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT /note= "signal peptide"
XX FT 24..207
XX FT /note= "mature protein"
XX
XX PN EP1041083-A1.
XX
XX PD 04-OCT-2000.
XX
XX PF 03-APR-2000; 2000EP-0107041.
XX
XX PR 01-APR-1999; 99JP-0095142.
XX
XX PA (ORIY) ORIENTAL YEAST CO LTD.
XX
XX PI Miyazaki K, Higashi S;
XX
XX DR WPI; 2000-603818/58.

XX
XX PT New modified tissue inhibitor of metalloproteinases, useful for
XX manufacturing compositions for inhibiting metastasis of cancer and
XX PT vascularisation and for preventing or treating diseases associated with
XX PT these, e.g. brain tumor -
XX
XX PS Disclosure; Page 12-13; 25pp; English.
XX
XX CC The present sequence represents an inhibitor of tissue metalloproteinase,
XX designated TIMP. The specification describes modified forms of TIMP,
XX CC where the amino-terminal alpha-amino group is modified with an electron
XX CC accepting group to substantially lose the ability to bind to a
XX CC metalloproteinase. Modified TIMP-2 prevents an accumulation of active
XX CC gelatinase. A on the cell surface, and can inhibit the activation of

CC precursor matrix metalloproteinases. The modified TIMP-2 and the
CC compositions comprising TIMP-2 are useful for inhibiting metastasis of
CC cancer and vascularisation. It is also used for treating diseases
CC associated with them. Specifically, these are useful for preventing or
CC treating metastasis of cancer of the stomach, colon, lung, head and
CC neck, brain tumour, breast, thyroid, prostate, ovary or pancreas, or
CC vascularisation or other conditions associated with these.

XX SQ Sequence 207 AA;
XX
XX Query Match 100.0%; Score 579; DB 21; Length 207;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-64;
XX Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLVQRYEIKMTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPTAFNCNSDLVIRAKFVGTPEVNTTLVQRYEIKMTKMYKGFQALGDAADIRF 83
QY 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWN 106
DB 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCFVAPWN 129

RESULT 11
AAM93377
ID AAM93377 standard; Protein; 207 AA.
XX
XX AC AAM93377;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human polypeptide, SEQ ID NO: 2953.
XX
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
XX OS Homo sapiens.
XX
XX PN EP1130094-A2.
XX
XX PD 05-SEP-2001.
XX
XX PF 07-JUL-2000; 2000EP-0114089.
XX
XX PR 08-JUL-1999; 99JP-0194486.
XX PR 11-JAN-2000; 2000JP-0118774.
XX PR 02-MAY-2000; 2000JP-0183765.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX DR WPI; 2001-524255/58.
XX
XX DR N-PSDB; AAK94297.
XX
XX PT 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
XX PS Claim 8; SEQ ID NO 2953; 1380pp + sequence listing; English.

XX
XX CC The invention relates to primers for synthesising full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesising the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesised by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence is a polypeptide
XX encoded by a full length human cDNA of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.

SQ Sequence 207 AA;
 Query Match 100.0%; Score 579; DB 22; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1,1e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 60
 DB 24 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 83
 QY 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSPVAPWN 106
 DB 84 VTPPMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSPVAPWN 129

RESULT 12

AAG89171
 ID AAG89171 standard; Protein, 207 AA.
 AAG89171;

DT 11-SEP-2001 (first entry)
 XX Human secreted protein, SEQ ID NO. 291.

DE Human secreted protein, SEQ ID NO. 291.
 KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
 KW GENSET.
 OS Homo sapiens.

XX MO200142451-A2.
 PN 14-JUN-2001.

PD 07-DEC-2000; 2000MO-1B01938.
 PF 08-DEC-1999; 99US-0169629.

PR 06-MAR-2000; 2000US-0187470.
 XX (GRST) GENSET.

PA (GRST) GENSET.
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
 XX WPI: 2001-367870/38.

DR N-PSDB; AAH64774.
 XX

PR Full length GENSET human nucleic acids encoding potentially secreted
 proteins, useful in gene therapy and vaccination against a variety of
 diseases, and for diagnosis of those diseases -
 XX

PS Claim 21; Page 825; 921pp; English.

CC The invention relates to full length GENSET human nucleic acids encoding
 CC potentially secreted proteins. The nucleic acids and the polypeptides
 CC they encode may be used in the prevention, treatment and diagnosis of
 CC diseases associated with inappropriate GENSET gene expression. For
 CC example, they be used to treat disorders associated with decreased
 CC GENSET gene expression by rectifying mutations or deletions in a
 CC patient's genome that affect the activity of GENSET or by supplementing
 CC the patient's own production of GENSET polypeptides. Conversely,
 CC antisense nucleic acid molecules may be administered to down regulate
 CC GENSET expression by binding with the cells' own genes and preventing
 CC their expression. The sense and antisense nucleic acids may also be
 CC used as DNA probes in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples, and hence to
 CC determine which patients may be in need of restorative therapy.
 CC The GENSET polypeptides may be used as antigens in the production of
 CC antibodies and in assays to identify modulators (agonists and
 CC antagonists) of GENSET polypeptide expression and activity. The
 CC present sequence is a GENSET polypeptide of the invention.

XX Sequence 207 AA;
 SQ

Query Match 100.0%; Score 579; DB 22; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1,1e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 60
 DB 24 CTCVPPHQTAFCSNDLVIRAKFVGTPEVNOTTLVQRYEIKMTKMYKGFQALGDAADIRF 83
 QY 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSPVAPWN 106
 DB 84 VTPPMESVCGYFHRSHNRSEEFLLAGKLQDGLHITTCSPVAPWN 129

RESULT 13

AAU99883
 ID AAU99883 standard; Protein, 522 AA.
 AAU99883;

AC AAU99883;
 DT 07-OCT-2002 (first entry)
 XX NTAP1 fusion protein.

DE NTAP1 fusion protein.
 XX NTAP1; Alzheimer's disease; tumour angiogenesis;
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
 KW cystic fibrosis; ocitis media; ocitis externa; HIV; psoriasis; eczema;
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
 KW glomerulonephritis; hypertension.

OS Homo sapiens.
 OS Synthetic.

FH Key Location/Qualifiers
 FT 2..127
 FT /note= "Human TIMP-1 amino acids 1-184"
 FT 128
 FT /note= "Linker methionine"
 FT 129..522
 FT /note= "Amino acids 1-394 of human AAT"

FT Region
 FT WO200250287-A2.
 PN 27-JUN-2002.
 PD 18-DEC-2001; 2001WO-US49256.
 PF 18-DEC-2000; 2000US-256699P.
 PR 20-NOV-2001; 2001US-331966P.
 XX (ARRI-) ARRIVA PHARM INC.

PA (ARRI-) ARRIVA PHARM INC.
 PI Barr PJ, Gibson HL, Pemberton P;
 XX WPI: 2002-500631/53.

DR N-PSDB; ABK88024.
 XX

PR Novel fusion protein useful for inhibiting protease activity associated
 with a disorder such as emphysema, asthma, comprises a first protease
 PR inhibitor comprising alpha 1-antitrypsin and a second protease
 PT inhibitor -
 PT
 XX Example 2; Page 87; 134pp; English.

PS This invention relates to a novel fusion protein comprising a first
 XX protease inhibitor comprising an alpha 1-antitrypsin or its functionally
 CC active portion and a second protease inhibitor or its functionally
 CC active protein. The fusion proteins of the invention may act as an
 CC inhibitor of protease activity. The fusion protein of the invention
 CC is useful for inhibiting protease activity associated with a disorder
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,
 CC cystic fibrosis, ocitis media, ocitis externa or HIV infection, or

CC for treating an individual suffering from or at risk for a disease or
 CC disorder involving unwanted protease activity. The proteins are useful
 CC for treating dermatological diseases such as atopic dermatitis, eczema
 CC and psoriasis, in inflammatory responses to viral infection, and for
 CC treating herpes infection, corneal or epidermal ulceration, chronic
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
 CC bacterial infection, Alzheimer's disease, hypertension and muscular
 CC dystrophy. The present sequence represents the NTAP1 fusion protein of
 CC the invention.

XX Sequence 522 AA;

Query Match 100.0%; Score 579; DB 23; Length 522;
 Best Local Similarity 100.0%; Pred. No. 3.5e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 60
 Db 2 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 61
 Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106
 Db 62 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 107

RESULT 14

AAU99885
 ID AAU99885 standard; Protein; 522 AA.

XX AAU99885;

XX 07-OCT-2002 (first entry)

XX rN-TAP1 fusion protein.

XX rN-TAP1; Alzheimer's disease; tumour angiogenesis;
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
 KW glomerulonephritis; hypertension.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Region 2..395 /note= "Human AAT amino acids 1-394"

FT Region 396

FT Region /note= "Linker methionine"

FT Region 397..522 /note= "Amino acids 1-126 of human TIMP-1"

XX WO200250287-A2.

XX 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US49256.

XX 18-DEC-2000; 2000US-256699P.

XX 20-NOV-2001; 2001US-331966P.

XX (ARRI-) ARRIVA PHARM INC.

XX Barr PJ, Gibson HL, Pemberton P;

XX WPI; 2002-500631/53.

XX N-PSDB; ABK8027.

XX Novel fusion protein useful for inhibiting protease activity associated

PT

PT inhibitor comprising alpha 1-antitrypsin and a second protease

XX inhibitor -

XX Example 3; Page 97; 134pp; English.

CC This invention relates to a novel fusion protein comprising a first
 CC protease inhibitor comprising an alpha 1-antitrypsin or its functionally
 CC active portion and a second protease inhibitor or its functionally
 CC active protein. The fusion proteins of the invention may act as an
 CC inhibitor of protease activity. The fusion protein of the invention
 CC is useful for inhibiting protease activity associated with a disorder
 CC such as emphysema, asthma, chronic obstructive pulmonary disease, or
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or
 CC for treating an individual suffering from or at risk for a disease or
 CC disorder involving unwanted protease activity. The proteins are useful
 CC for treating dermatological diseases such as atopic dermatitis, eczema
 CC and psoriasis, in inflammatory responses to viral infection, and for
 CC treating herpes infection, corneal or epidermal ulceration, chronic
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
 CC bacterial infection, Alzheimer's disease, hypertension and muscular
 CC dystrophy. The present sequence represents the rN-TAP1 fusion protein of
 CC the invention.

XX Sequence 522 AA;

Query Match 100.0%; Score 579; DB 23; Length 522;
 Best Local Similarity 100.0%; Pred. No. 3.5e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 60
 Db 397 CTCVPPHPQTAFNCNSDLVIRAKFVGTPEVNTTLQRYEIKMTKMYKGFQALGDAADIRF 456

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106

Db 457 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 502

RESULT 15

AAU99882

ID AAU99882 standard; Protein; 580 AA.

XX AAU99882;

XX 07-OCT-2002 (first entry)

XX TAP1 fusion protein.

DE TAP1; Alzheimer's disease; tumour angiogenesis;

KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;

KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;

KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;

KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;

KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;

XX glomerulonephritis; hypertension.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Region 2..185 /note= "Human TIMP-1 amino acids 1-184"

FT Region 186

FT Region /note= "Linker methionine"

FT Region 187..580

FT Region /note= "Amino acids 1-394 of human AAT"

XX WO200250287-A2.

XX 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US49256.
 PF
 XX 18-DEC-2000; 2000US-256699P.
 PR
 PR 20-NOV-2001; 2001US-331966P.
 XX
 XX (ARRI-) ARRIVA PHARM INC.
 PA
 XX
 PI Barr PJ, Gibson HL, Pemberton P;
 XX
 DR MPI: 2002-500631/53.
 DR N-PSDB; ABK88023.

XX Novel fusion protein useful for inhibiting protease activity associated
 PT with a disorder such as emphysema, asthma, comprises a first protease
 PT inhibitor comprising alpha 1-antitrypsin and a second protease
 PT inhibitor -
 XX

XX Example 1; Page 79-82; 134pp; English.

CC This invention relates to a novel fusion protein comprising a first
 CC protease inhibitor comprising an alpha1-antitrypsin or its functionally
 CC active portion and a second protease inhibitor or its functionally
 CC active protein. The fusion proteins of the invention may act as an
 CC inhibitor of protease activity. The fusion protein of the invention
 CC is useful for inhibiting protease activity associated with a disorder
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or
 CC for treating an individual suffering from or at risk for a disease or
 CC disorder involving unwanted protease activity. The proteins are useful
 CC for treating dermatological diseases such as atopic dermatitis, eczema
 CC and psoriasis, in inflammatory responses to viral infection, and for
 CC treating herpes infection, corneal or epidermal ulceration, chronic
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
 CC bacterial infection, Alzheimer's disease, hypertension and muscular
 CC dystrophy. The present sequence represents the TAPI fusion protein of
 CC the invention.
 CC
 XX

XX Sequence 580 AA;

Query Match 100.0%; Score 579; DB 23; Length 580;
 Best Local Similarity 100.0%; Pred. No. 4e-64;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 CTCVPPHPOTAFQNSDLVIRAKFVGTPENVQTTLYRYEIKMTKMYKGFQALGDADIRF 60
 |||
 2 CTCVPPHPOTAFQNSDLVIRAKFVGTPENVQTTLYRYEIKMTKMYKGFQALGDADIRF 61
 |||
 0Y 61 VYTPAMESYCGYFHRSHNSSEFLINAGKLODGLHITTCSPVAPWN 106
 |||
 DB 62 VYTPAMESYCGYFHRSHNSSEFLINAGKLODGLHITTCSPVAPWN 107
 |||

Search completed: December 17, 2002, 15:06:04
 Job time : 23.7586 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 10.6 Seconds
(without alignments)
961.344 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579

Sequence: 1 CTCVPHPHQAFNCNSDIVIR.....GKLQDGLLHTTCSFVAPWN 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	207	1	ZYHUP metalloproteinase
2	579	100.0	207	1	UC4303 matrix metalloprot
3	508	87.7	207	1	A35685 metalloproteinase
4	507	87.6	206	1	A33350 metalloproteinase
5	504	87.0	207	2	I46964 metalloproteinase
6	504	87.0	207	2	I47061 metalloproteinase
7	458	79.1	205	1	A26106 collagenase inhibi
8	446	77.0	217	1	UC2557 metalloproteinase
9	234	40.4	220	1	A37128 metalloproteinase
10	233	40.2	196	1	S38624 metalloproteinase
*11	233	40.2	220	1	JH0683 metalloproteinase
12	233	40.2	220	1	S45683 metalloproteinase
13	233	40.2	220	2	I53415 metalloproteinase
14	227	39.2	220	2	I53415 metalloproteinase
15	218	37.7	212	1	A35996 metalloproteinase
16	215	37.1	211	1	A43429 metalloproteinase
17	212	36.6	211	1	S45317 metalloproteinase
18	212	36.6	211	1	A53532 metalloproteinase
19	74.5	12.9	50	2	UC4630 metalloproteinase
20	74	12.8	158	2	I53729 metalloproteinase
21	72	12.4	530	2	F89123 metalloproteinase
22	69	11.9	345	1	NBMS probable Tail-Like
23	67.5	11.7	421	2	T19315 apolipoprotein H p
24	66.5	11.5	490	2	F82973 hypothetical prote
25	66	11.4	464	2	E82517 betaine aldehyde d
26	66	11.4	572	2	UC5317 hypothetical prote
27	66	11.4	597	2	A82666 dihydropyrimidinase
28	65	11.2	2549	2	A54837 rapamycin/FKBP12 c
29	64.5	11.1	195	2	AF1496 hypothetical prote

30	64.5	11.1	1005	2	T31333 beta-galactosidase
31	64	11.1	187	2	S25395 H+-transporting tw
32	64	11.1	932	2	UC5953 inter-alpha-inhibi
33	63.5	11.0	403	2	B71378 probable recf prot
34	63.5	11.0	1118	2	S57833 transmembrane prot
35	63	10.9	387	2	A86322 F6A14.9 protein -
36	63	10.9	572	2	S58889 collagen response
37	63	10.9	1056	2	T33167 hypothetical prote
38	63	10.9	1123	1	WMBEH7 U137 protein - hum
39	62	10.7	433	1	B65058 f15C protein homol
40	62	10.7	698	2	H71535 hypothetical prote
41	62	10.7	1426	2	T00337 hypothetical prote
42	62	10.7	1799	2	AD1895 serine/threonine k
43	61.5	10.6	250	2	G83276 precorrin-3 methyl
44	61.5	10.6	332	2	UC5465 2,3-dihydroxydiphe
45	61.5	10.6	562	2	A96773 hypothetical prote

ALIGNMENTS

RESULT 1
ZYHUP metalloproteinase tissue inhibitor 1 precursor (validated) - human
N:Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor
C:Species: Homo sapiens (man)
C:Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000
C:Accession: A93372; A93363; A20554; A20555; A35826; A48417; S20318; S15872; I52912; S664
R:DoCherty, A.O.P.; Lyons, A.; Smith, B.U.; Wright, E.M.; Stephens, P.E.; Harris, T.O.R.;
Nature 318, 66-69, 1985
A:Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to ery
A:Reference number: A93372; MUID:86040463; PMID:3903517
A:Accession: A93372
A:Molecule type: mRNA
A:Residues: 1-207 <DOC>
A:Cross-references: GB:X03124; NID:G37182; PIDN:CAA26902.1; PID:G37183
R:Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.;
Nature 315, 768-771, 1985
A:Title: Molecular characterization and expression of the gene encoding human erythroid-1
A:Reference number: A93363; MUID:85240567; PMID:3838290
A:Accession: A93363
A:Molecule type: mRNA
A:Residues: 1-207 <GAS>
R:Camichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H.G.
Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986
A:Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
A:Reference number: A23534; MUID:86205964; PMID:3010309
A:Accession: A23534
A:Molecule type: mRNA
A:Residues: 1-207 <CAR>
A:Cross-references: GB:M12670; NID:G182482; PIDN:AAA52436.1; PID:G182483
A:Note: parts of this sequence were confirmed by protein sequencing
A:Note: carbohydrate binding sites were determined
R:Stricklin, G.P.; Welgus, H.G.
J. Biol. Chem. 258, 12252-12258, 1983
A:Title: Human skin fibroblast collagenase inhibitor.
A:Reference number: A20595; MUID:84032401; PMID:6313647
A:Accession: A20595
A:Molecule type: protein
A:Residues: 24-44, 'L', 46 <STR>
A:Note: six disulfide bonds are present
R:Rapp, G.; Frudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.
DNA Cell Biol. 9, 479-485, 1990
A:Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.
A:Reference number: A35826; MUID:91025550; PMID:2171551
A:Accession: A35826
A:Molecule type: mRNA
A:Residues: 1-207 <RAP>
A:Cross-references: GB:M8188
R:Van Ransst, M.; Norga, K.; Masure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van I
Cytokine 3, 231-239, 1991
A:Title: The cytokine-protease connection: identification of a 96-kD TGF-1 gelatinase and
A:Reference number: A48417; MUID:91355647; PMID:1653055

A:Accession: A48417
A:Molecule type: protein
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-52 <VAN>
A:Experimental source: monocytic cell line THP-1
A:Note: sequence modified after extraction from NCBI backbone
A:Note: sequence incorrectly identified as 96K gelatinase
R:Osrhues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.
FEBS Lett. 296, 16-20, 1992
A:Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)
A:Reference number: S20318; MUID:92111776; PMID:1730286
A:Accession: S20318
A:Molecule type: protein
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-38 <OST>
A:Experimental source: rheumatoid synovial fluid
R:Opdenakker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.
FEBS Lett. 284, 73-78, 1991
A:Title: Natural human monocyte gelatinase and its inhibitor.
A:Reference number: S15872; MUID:91285112; PMID:1647974
A:Accession: S15872
A:Molecule type: protein
A:Residues: 'X', 25, 'X', 27-35, 'X', 37-42, 'X', 44, 'X', 46, 'X', 48-51 <FEB>
A:Experimental source: peripheral blood monocytes
R:Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;
Biochem. J. 268, 267-274, 1990
A:Title: Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIMP)
A:Reference number: A38978; MUID:90303199; PMID:2163605
A:Contents: annotation; disulfide bonds
R:Opbroek, A.; Kenney, M.C.; Brown, D.
Curr. Eye Res. 12, 877-883, 1993
A:Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).
A:Reference number: I52912; MUID:94123576; PMID:7507419
A:Accession: I52912
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-207 <RES>
A:Cross-references: GB:S68252; NID:G545022; PIDN:AA014009.1; PID:G4261709
R:Triebel, S.; Blaeser, J.; Gore, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Tschesche, H.
Eur. J. Biochem. 231, 714-719, 1995
A:Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol
A:Reference number: S66461; MUID:95377303; PMID:7649172
A:Accession: S66461
A:Molecule type: protein
A:Residues: 24-38 <TRI>
A:Experimental source: polymorphonuclear leukocytes
C:Comment: This protein, found in a variety of body fluids, complexes with metalloprotei
s-specific, stimulating the growth and differentiation of only human and murine erythro
C:Comment: The remarkable heat stability of this protein may be due to disulfide bond fo
C:Genetics:
A:Gene: GDB:TIMP1; CLGI; TIMP
A:Cross-references: GDB:I19615; OMTM:305370
A:Map position: Xp11.3-Xp11.23
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; glycoprotein; metalloproteinase inhibitor
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <WAT>
F:24-93,26-122,36-147,150-197,155-160,168-189/Disulfide bonds: #status experimental
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 579; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.3e-58;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 2
JC4303

matrix metalloproteinase-1 tissue inhibitor - baboon
C:Species: Papio sp. (baboon)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 16-Jul-1999
C:Accession: JC4303
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.
Gene 163, 267-271, 1995
A:Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of
A:Reference number: JC4303; MUID:96011646; PMID:7590279
A:Accession: JC4303
A:Molecule type: mRNA
A:Residues: 1-207 <FOR>
A:Cross-references: GB:L37295; NID:G561545; PIDN:AAA99943.1; PID:G561546
A:Experimental source: smooth muscle cell
C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase f
se and influences the proteinase activity. It has a role as a physiological molecule f
C:Genetics:
A:Gene: timp-1
C:Superfamily: metalloproteinase inhibitor
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 579; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.3e-58;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 60
Db 24 CTCVPPHPQTAFCSNLDLVIKAFVGTPEVNTTLYQRYEIKMTKMYKGFQALGDAADIRF 83

Qy 61 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 106
Db 84 VYTPAMESVCGYFHRSHNRSEFLIAGKLDGLLHITTCSFVAPWN 129

RESULT 3
A35685
Metalloproteinase inhibitor 1 precursor - bovine
N:Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhib
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C:Accession: A35685; B34468; B29712; A34833; I46979
R:Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 171, 250-256, 1990
A:Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression
A:Reference number: A35685; MUID:90365711; PMID:2393392
A:Accession: A35685
A:Molecule type: mRNA
A:Residues: 1-207 <PRE>
A:Cross-references: GB:M60073; NID:G163760; PIDN:AAA30784.1; PID:G163761
A:Experimental source: ovary cDNA library
R:De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.
J. Biol. Chem. 264, 17445-17453, 1989
A:Title: Purification and characterization of two related but distinct metalloproteinase
A:Reference number: A34468; MUID:90008914; PMID:2551903
A:Accession: B34468
A:Molecule type: protein
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>
A:Experimental source: culture medium of aortic endothelial cells
R:Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Streech,
Bio/Technology 5, 595-598, 1987
A:Title: Molecular cloning and synthesis of biologically active human tissue inhibitor
A:Reference number: A29712
A:Accession: B29712
A:Molecule type: protein
A:Residues: 24-37 <KAC>
A:Experimental source: culture medium of fibroblastic BC 21 cells
A:Note: protein inhibits angiogenesis
R:Moses, M.A.; Sudhalter, J.; Langer, R.
Science 248, 1408-1410, 1990
A:Title: Identification of an inhibitor of neovascularization from cartilage.
A:Reference number: A34833; MUID:90288433; PMID:1694043
A:Accession: A34833
A:Molecule type: protein

A:Residues: 24-51 <MOS>
A:Experimental source: cartilage
R:Sachh, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.
Biol. Reprod. 50: 835-844, 1994
A:Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct
A:Reference number: 146979; MUID:94257757; PMID:8199264
A:Accession: 146979
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <SAT>
A:Cross-references: GB:S70841; NID:9546973; PIDN:AA330892.1; PID:9546974
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases
A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agents
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:1-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F:93-26-122-36-147-150-155-160-168-189/Diulfide bonds: #status predicted
F:53,101/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 87.7%; Score 508; DB 1; Length 207;
Best Local Similarity 86.8%; Pred. No. 5,9e-50;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 60
Db 24 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 83
Oy 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106
Db 84 ITPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 129

RESULT 4

A33350
A:Title: metalloproteinase inhibitor 1 precursor - rabbit
N:Alternate names: TIMP-1; tissue inhibitor of metalloproteinases 1
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Jun-1992 #sequence revision 12-Apr-1996 #text_change 18-Jun-1999
C:Accession: A33350; A30864
R:Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter, R.H.; Quidle, D.J.
J. Biol. Chem. 264: 7092-7095, 1989
A:Title: Hyperoxic exposure alters gene expression in the lung. Induction of the tissue inhibitor of metalloproteinase 1
A:Reference number: A33350; MUID:89214135; PMID:2708356
A:Accession: A33350
A:Molecule type: mRNA
A:Residues: 1-206 <HOR>
A:Cross-references: GB:J04712; NID:9165742; PIDN:AAA31478.1; PID:9165743
A:Experimental source: hyperoxia-exposed lung of New Zealand white rabbits
C:Comment: Expression of this protein in the lung is induced 6-fold by hyperoxia.
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases
A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agents
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patterns
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-206/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
F:24-93-26-122-36-147-150-155-160-168-188/Diulfide bonds: #status predicted
F:53,101/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 87.6%; Score 507; DB 1; Length 206;
Best Local Similarity 86.8%; Pred. No. 7,6e-50;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 60
Db 24 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 83

Oy 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106
Db 84 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 129

RESULT 5

146964
A:Title: metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 19-Jan-2001
C:Accession: 146964
R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.
Endocrinology 134, 344-352, 1994
A:Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: or
eal tissue.
A:Reference number: 146964; MUID:94102210; PMID:8275949
A:Accession: 146964
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <SMI>
A:Cross-references: GB:S67450; NID:9456989; PIDN:AB29472.1; PID:9456990
C:Superfamily: metalloproteinase inhibitor

Query Match 87.0%; Score 504; DB 2; Length 207;
Best Local Similarity 85.8%; Pred. No. 1,7e-49;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 60
Db 24 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 83
Oy 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106
Db 84 ITPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 129

RESULT 6

147061
A:Title: collagenase inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1997 #sequence revision 04-Sep-1997 #text_change 16-Jul-1999
C:Accession: 147061
R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.
Mol. Cell. Endocrinol. 83, 65-71, 1992
A:Title: Differential screening of ovarian cDNA libraries detected the expression of the
tissue inhibitor of metalloproteinase 1
A:Reference number: 147061; MUID:92201478; PMID:1312961
A:Accession: 147061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TN>
A:Cross-references: GB:S86211; NID:9247729; PIDN:AB21865.1; PID:9247730
C:Superfamily: metalloproteinase inhibitor

Query Match 87.0%; Score 504; DB 2; Length 207;
Best Local Similarity 85.8%; Pred. No. 1,7e-49;
Matches 91; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 60
Db 24 CTCVPHPHQTACNSDVLVIRAFVGTPEVNOITLYORIEIKTKTKYKGOALGDAADIRF 83
Oy 61 VTPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 106
Db 84 ITPPMESVCGYFHRSHNRSEEFLLAGKLDGDLHITTCSPFAPWN 129

RESULT 7

A26106
A:Title: metalloproteinase inhibitor 1 precursor - mouse
N:Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor
C:Species: Mus musculus (house mouse)
C:Date: 05-Oct-1988 #sequence revision 12-Apr-1996 #text_change 18-Jun-1999
C:Accession: A26106; A26106; A05276

J. Biol. Chem. 264, 17374-17378, 1989
 A>Title: Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metalloprote
 A:Reference number: A34464; MUID:90008902; PMID:2793861
 A:Accession: A34464
 A:Molecule type: protein
 A:Residues: 27-77, 'K', '79-81, 'I', '83-100, 'E', '102-117, '119-121, 'R', '123-149, 'Q', '151-174, 'T', '1
 A:Experimental source: serum-free culture medium of A2058 cells
 R:Goldberg, G.I.; Warner, B.L.; Grant, G.A.; Eissen, A.Z.; Wilhelm, S.; He, C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 8207-8211, 1989
 A>Title: Human 72-kilodalton type IV collagenase forms a complex with a tissue inhibitor
 A:Reference number: A34415; MUID:90046765; PMID:2554304
 A:Accession: A34415
 A:Molecule type: protein
 A:Residues: 30-51, '124-141, '159-173 <COL>
 R:Malik, K.; Sejima, H.; Aoki, T.; Iwata, K.
 submitted to the EMBL Data Library, August 1990
 A>Description: Nucleotide sequence of a TIMP-II cDNA.
 A:Reference number: S21303
 A:Accession: S21303
 A:Molecule type: mRNA
 A:Residues: 30-95, 'V', '97-214 <MAL>
 A:Cross-references: EMBL:X54533; NID:937180; PIDN:CAA38400.1; PID:G37181
 R:Oshues, A.; Knauper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.
 FEBS Lett. 296, 16-20, 1992
 A>Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP
 A:Reference number: S20318; MUID:92111776; PMID:1730286
 A:Accession: S20318
 A:Molecule type: protein
 A:Residues: 'X', '28, 'X', '30-38, 'X', '40-41 <OST>
 A:Experimental source: rheumatoid synovial fluid
 R:Ward, R.V.; Hemby, R.M.; Reynolds, J.J.; Murphy, G.
 Biochem. J. 278, 179-187, 1991
 A>Title: The purification of tissue inhibitor of metalloproteinases-2 from its 72 kDa pr
 A:Reference number: S17165; MUID:91354200; PMID:1909113
 A:Accession: S17165
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27, 'X', '29, 'X', '31-38 <WAR>
 R:Ohba, Y.; Goto, Y.; Kimura, Y.; Suzuki, F.; Hisa, T.; Takahashi, K.; Takigawa, M.
 Biochim. Biophys. Acta 1245, 1-8, 1995
 A>Title: Purification of an angiogenesis inhibitor from culture medium conditioned by a
 A:Reference number: S58794; MUID:9538380; PMID:754625
 A:Accession: S58794
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-37 <OHBA>
 C:Genetics:
 A:Gene: GDB:TIMP2
 A:Cross-references: GDB:132612; OMIM:188825
 A:Map position: 17q25-17q25
 C:Function:
 A>Description: regulation of extracellular matrix remodeling by inhibition of matrix met
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
 C:Superfamily: metalloproteinase inhibitor
 C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
 F.1-26/Domain: signal sequence #status predicted <SIG>
 F.127-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>
 F.127-98, '29-127, '39-152, '154-201, '159-164, '172-193/Diulfide bonds: #status predicted

Query Match 40.4%; Score 234; DB 1; Length 220;
 Best Local Similarity 44.7%; Pred. No. 7, 2e-19;
 Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

OY 1 CTCVPHPTACNSDLVIRAKFVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53
 DB 27 CSCSPVHPQACNADVIRAKVSEKVDSDNDYGNPKIKYQIEIKQKFK-----G 81

OY 54 DADIRFVYTPMSEVCGYFHRSHNRSEFLIAGKIQ-DGLHITTCSPVAPWN 106
 DB 82 PKDIEFIYTPASSAVCG-VSLDVGKKEVYLAGKAEKGKMHITLCPFIVPWD 134

RESULT 10

S38624
 metalloproteinase inhibitor 2 precursor - long-tailed hamster (fragment)
 N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
 C:Species: Cricetus longicaudatus (long-tailed hamster)
 C>Date: 06-Jan-1995 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C:Accession: S38624
 R:Suzuki, Y.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S38624
 A:Accession: S38624
 A:Molecule type: mRNA
 A:Residues: 1-196 <SUZ>
 A:Cross-references: EMBL:X75924; NID:9414876; PIDN:CAA53528.1; PID:G414877
 C:Function:
 A>Description: regulation of extracellular matrix remodeling by inhibition of matrix met
 possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
 C:Superfamily: metalloproteinase inhibitor
 C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
 F.3-196/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
 F.3-74, '5-103, '15-128, '130-177, '135-140, '148-169/Diulfide bonds: #status predicted

Query Match 40.2%; Score 233; DB 1; Length 196;
 Best Local Similarity 44.7%; Pred. No. 8, 2e-19;
 Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

OY 1 CTCVPHPTACNSDLVIRAKFVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53
 DB 3 CSCSPVHPQACNADVIRAKVSEKVDSDNDYGNPKIKYQIEIKQKFK-----G 57

OY 54 DADIRFVYTPMSEVCGYFHRSHNRSEFLIAGKIQ-DGLHITTCSPVAPWN 106
 DB 58 PKDIEFIYTPASSAVCG-VSLDVGKKEVYLAGKAEKGKMHITLCPFIVPWD 110

RESULT 11

JH0683
 metalloproteinase inhibitor 2 precursor - mouse
 N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 R:Shimizu, S.; Malik, K.; Sejima, H.; Kishii, J.; Hayakawa, T.; Koiwai, O.
 Gene 114, 291-292, 1992
 A>Title: Cloning and sequencing of the cDNA encoding a mouse tissue inhibitor of metallo
 A:Reference number: JH0683; MUID:92290292; PMID:1601312
 A:Accession: JH0683
 A:Molecule type: mRNA
 A:Residues: 1-220 <SHI>
 A:Cross-references: EMBL:X62622; NID:954801; PIDN:CAA44491.1; PID:954802
 A:Experimental source: 3T3 fibroblast strain Balb/c
 R:Leeco, K.U.; Hayden, L.U.; Sharma, R.R.; Rochelleau, H.; Greenberg, A.H.; Edwards, D.R.
 Gene 117, 209-217, 1992
 A>Title: Differential regulation of TIMP-1 and TIMP-2 mRNA expression in normal and Ha-r
 A:Reference number: JCI1234; MUID:92347695; PMID:1639268
 A:Accession: JCI1234
 A:Molecule type: mRNA
 A:Residues: 1-11, 'H', '13-20, 'L', '22-194, 'E', '196-220 <LEC>
 A:Cross-references: GB:M93954; NID:9202053; PIDN:AAA40446.1; PID:9202054
 R:Kishii, J.
 Matrix 11, 373, 1991
 A>Title: Correction.
 A:Reference number: S18428; MUID:92244125; PMID:1667327
 A:Accession: S18428
 A:Molecule type: protein
 A:Residues: 27-46, 'H', '48-50-53, 'VD', '56, 'DY' <KIS>
 R:Kishii, J.I.; Ogawa, K.; Yamamoto, S.; Hayakawa, T.
 Matrix 11, 10-16, 1991
 A>Title: Purification and characterization of a new tissue inhibitor of metalloproteinase
 A:Reference number: S15987; MUID:91226375; PMID:1851244
 A:Accession: S15987
 A:Molecule type: protein
 A:Residues: 27-46, 'HLX', '50-52, 'LX', '55-56, 'DXX', '60, 'X', '62 <KIS>
 A>Note: this sequence has been revised in reference S18428

[illegible]

Job time : 11.6 secs

C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F:27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 39.2%; Score 227; DB 1; Length 220;

Best Local Similarity 43.9%; Pred. No. 4,5e-18;
Matches 50; Conservative 16; Mismatches 34; Indels 14; Gaps 5;

QY 1 CTCVPPHQTAFNCNSDLVIRAKVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 53
Db 27 CSCSPVHPQOACNCNDIVIRAKVAKKEVDGNDYGNPKRIQYIKQIKMFK-----G 81
QY 54 DAADIRFYTPAMESVCGYFRSHNRSEFLIAGKLQ-DGLHITTCGTFVAPWN 106
82 PDQIEFYTPAFAAVCG-VSLDIGGKEYLIAGKAGNGNMHITLCPFIVPWD 134

RESULT 15

A43429
metalloproteinase inhibitor 3 precursor - chicken
N:Alternate names: 21K extracellular matrix protein; TIMP-3; tissue inhibitor of metallo
C:Species: Gallus gallus (chicken)
C:Date: 04-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C:Accession: A43429; A39043
R:Pavloff, N.; Staskus, P.W.; Kishanani, N.S.; Hawkes, S.P.
J. Biol. Chem. 267, 17321-17326, 1992
A:Title: A new inhibitor of metalloproteinases from chicken: ChIMP-3. A third member of
A:Reference number: A43429; MUID:92381050; PMID:1512267
A:Accession: A43429

A:Molecule type: mRNA

A:Residues: 1-212 <PAV>

A:Cross-references: GB:M94531; NID:G211901; PIDN:AAA48813.1; PID:G211902

A:Experimental source: ten-day old embryo cDNA library

A>Note: Sequence extracted from NCBI backbone (NCBIN:111960, NCBIPI:111961)

R:Staskus, P.W.; Maslusz, F.R.; Pallanck, L.J.; Hawkes, S.P.

J. Biol. Chem. 266, 449-454, 1991

A:Title: The 21-kDa protein is a transformation-sensitive metalloproteinase inhibitor of
A:Reference number: A39043; MUID:91093162; PMID:1845973

A:Accession: A39043

A:Molecule type: protein

A:Residues: 26-51, 'I', 53 <STH>

A:Experimental source: cultured embryonic fibroblasts infected with Rous sarcoma virus

A>Note: contains disulfide bonds; not glycosylated; has inhibitory activity

C:Function:

A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met
A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C:Superfamily: metalloproteinase inhibitor
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-212/Product: metalloproteinase inhibitor 3 #status experimental <MAT>
F:25-92,27-119,37-144,146-193,151-156,164-185/Disulfide bonds: #status predicted
F:208/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match 37.7%; Score 218; DB 1; Length 212;

Best Local Similarity 40.2%; Pred. No. 4,5e-17;
Matches 43; Conservative 21; Mismatches 37; Indels 6; Gaps 3;

QY 1 CTCVPPHQTAFNCNSDLVIRAKVGTPEVNO-TTLVQ-----RYEIKMTKMYKGFQALG 59
Db 25 CTCVPIHPQDACNSDIVIRAKVAGKLMKDPFGTMRVYTKQMKYRGFOIM---PHVQ 81

QY 60 FVYTPAMESVCGYFRSHNRSEFLIAGKLQDGLHITTCGTFVAPWN 106
Db 82 YITPASESLCGV--KLEVNKYQYLITGRVYEGKYVTGLCNWYKMD 126

Search completed: December 17, 2002, 15:07:10

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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:26 ; Search time 5.84828 Seconds
(without alignments)
751.756 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579
Sequence: 1 CTCVPPHPQTAFCNSDLVIR.....GKLDPGLHITTCSEFVAPWN 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	207	1	TIM1_HUMAN
2	579	100.0	207	1	TIM1_PAPCY
3	569	98.3	207	1	TIM1_MACMU
4	508	87.7	207	1	TIM1_BOVIN
5	507	87.6	206	1	TIM1_RABIT
6	504	87.0	207	1	TIM1_SHEEP
7	500	86.4	207	1	TIM1_FIG
8	477	82.4	207	1	TIM1_HORSE
9	458	79.1	205	1	TIM1_MOUSE
10	455	78.6	207	1	TIM1_CANFA
11	446	77.0	217	1	TIM1_RAT
12	235	40.6	214	1	TIM3_SCYTO
13	234	40.4	220	1	TIM2_CAVPO
14	234	40.4	220	1	TIM2_HUMAN
15	233	40.2	196	1	TIM2_CRILLO
16	233	40.2	220	1	TIM2_MOUSE
17	229	38.6	220	1	TIM2_RAT
18	229	38.6	220	1	TIM2_CANFA
19	228	39.4	194	1	TIM2_RABIT
20	227	39.2	220	1	TIM2_BOVIN
21	219	37.8	220	1	TIM2_CHICK
22	218	37.7	212	1	TIM3_CHICK
23	215	37.1	211	1	TIM3_HORSE
24	215	37.1	211	1	TIM3_HUMAN
25	213	36.8	214	1	TIM3_XENLA
26	212	36.6	211	1	TIM3_MOUSE
27	212	36.6	211	1	TIM3_RAT
28	210.5	36.4	224	1	TIM4_MOUSE
29	210	36.3	211	1	TIM4_BOVIN
30	208.5	36.0	224	1	TIM4_RAT
31	201.5	34.8	224	1	TIM4_HUMAN
32	155	26.8	151	1	TIM3_RABIT
33	140.5	24.3	107	1	TIM4_BOVIN

34	140.5	24.3	170	1	TIM4_RABIT	O97591 oryctolagus
35	137.5	23.7	91	1	TIM2_HORSE	O77117 equus caball
36	100	17.3	210	1	TIMP_DROME	O97114 drosophila
37	69	11.9	345	1	APOH_MOUSE	O01339 mus musculus
38	67.5	11.7	421	1	NXF2_CABEL	O9758 caenorhabdi
39	66	11.4	572	1	DPY2_BOVIN	O02675 bos taurus
40	66	11.4	572	1	DPY2_HUMAN	O16555 homo sapien
41	65	11.2	2549	1	FRAP_MOUSE	O91199 mus musculus
42	65	11.2	2549	1	FRAP_RAT	P42346 rattus norv
43	64.5	11.1	1005	1	BGAL_ACTPL	P70753 actinobacil
44	64	11.1	187	1	ATPD_ODOSI	O00821 odontocela s
45	63.5	11.0	352	1	RECF_TREPA	O83049 treponema p

ALIGNMENTS

RESULT 1
TIM1_HUMAN STANDARD; PRT; 207 AA.
AC P01033; Q14252; Q9UCU1;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid
potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases)
DE (Fibroblast collagenase inhibitor) (Collagenase inhibitor).
GN TIMP1 OR TIMP OR CLGI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86040463; PubMed=3903517;
RA Docherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,
RA Harris T.J.R., Murphy G., Reynolds J.J.;
RT "Sequence of human tissue inhibitor of metalloproteinases and its
RT identity to erythroid-potentiating activity.";
RL Nature 318:66-69(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85240567; PubMed=3839290;
RA Gasson J.C., Golde D.W., Kaufman S.E., Westbrook C.A., Hewick R.M.,
RA Kauffman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,
RA Orr E.C., Clark S.C.;
RT "Molecular characterization and expression of the gene encoding human
RT erythroid-potentiating activity.";
RL Nature 315:768-771(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205964; PubMed=3010309;
RA Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,
RA Welgus H.G., Stricklin G.P.;
RT "Primary structure and cDNA cloning of human fibroblast collagenase
RT inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205964; PubMed=3010309;
RA Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,
RA Welgus H.G., Stricklin G.P.;
RT "Primary structure and cDNA cloning of human fibroblast collagenase
RT inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025550; PubMed=2171551;
RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
RA Scheit K.H.;
RT "Characterization of three abundant mRNAs from human ovarian
RL granulosa cells.";
RL DNA Cell Biol. 9:479-485(1990).


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AC PA9061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9556;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Arteria;
RX MEDLINE=96011646; PubMed=7590279;
RA Forough R., Nikkari S.T., Hasenstab D., Ilea H., Clowers A.W.;
RT "Cloning and characterization of a cDNA encoding the baboon tissue
inhibitor of matrix metalloproteinase-1 (TIMP-1).";
R1 Gene 163:267-271(1995).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L37295; AAA99943.1; -
DR HSSP; P01033; ID2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SMO0206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23213 MW; 5AE4FDBEAB2BCDC CRC64;
Query Match 100.0%; Score 579; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 2,5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTCVPPHPOTAFCSNDLVIRAKVGTPEVNOITLYQRYEIKTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPOTAFCSNDLVIRAKVGTPEVNOITLYQRYEIKTKMYKGFQALGDAADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLODGLHITTCSPFAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLODGLHITTCSPFAPWN 129
RESULT 3
ID TIM1_MACMU STANDARD; PRT; 207 AA.
AC Q95KL9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ji S., Wang Y., Li H., Ji W., Piao Y.;
RT "Cloning and characterization of tissue inhibitor of matrix
metalloproteinase-1 (TIMP-1) cDNA from Macaca mulatta.";
R1 Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
DR EMBL; AF363397; AAK53704.1; -
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; FALSE_NEG.
KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23247 MW; 4EE227D2AAB8580 CRC64;
Query Match 98.3%; Score 569; DB 1; Length 207;
Best Local Similarity 99.1%; Pred. No. 3,6e-58;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTCVPPHPOTAFCSNDLVIRAKVGTPEVNOITLYQRYEIKTKMYKGFQALGDAADIRF 60
DB 24 CTCVPPHPOTAFCSNDLVIRAKVGTPEVNOITLYQRYEIKTKMYKGFQALGDAADIRF 83
QY 61 VYTPMESVCGYFHRSHNRSEEFLLAGKLODGLHITTCSPFAPWN 106
DB 84 VYTPMESVCGYFHRSHNRSEEFLLAGKLODGLHITTCSPFAPWN 129
RESULT 4
ID TIM1_BOVIN STANDARD; PRT; 207 AA.
AC P20414; Q9TVB0;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-
1).
GN TIMP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90365711; PubMed=2393392;
RA Preudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;
RT "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and
RT expression in bovine ovarian tissue.";
RL Biochem. Biophys. Res. Commun. 171:250-256(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9425757; PubMed=8199264;
RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;
RT "Tissue inhibitor of metalloproteinases (TIMP-1) produced by
RT granulosa and oviduct cells enhances in vitro development of bovine
RT embryo.";
RL Biol. Reprod. 50:835-844(1994).
RN [3]
RP SEQUENCE OF 25-191 FROM N.A.
RC TISSUE=Skeletal muscle;
RA Balcerzak D., Queregeesser L., Dixon W.T., Baracos V.E.;
RT "Involvement of fibroblasts and muscle cells in the expression of an
RT extracellular proteolytic cascade in bovine skeletal muscle.";
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 24-69.
RX MEDLINE=90008914; PubMed=2551903;
RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
RT "Purification and characterization of two related but distinct
RT metalloproteinase inhibitors secreted by bovine aortic endothelial
RT cells.";
RL J. Biol. Chem. 264:17445-17453(1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
DR EMBL; M60073; AAA30784.1; -.
DR EMBL; S70841; AAB30892.1; -.
DR EMBL; AF144763; AAD30303.1; -.
DR PIR; A35685; A35685.
DR PIR; B34468; B34468.
DR HSSP; P01033; IUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 207 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 147 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 207 AA; 23031 MW; E672BEE2B865F3F7 CRC64;
Query Match 87.7%; Score 508; DB 1; Length 207;
Best Local Similarity 86.8%; Pred. No. 4.8e-51;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
MEDLINE=90365711; PubMed=2393392;
Preudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;
"mRNA of bovine tissue inhibitor of metalloproteinase: sequence and
expression in bovine ovarian tissue.";
Biochem. Biophys. Res. Commun. 171:250-256(1990).
[2]
SEQUENCE FROM N.A.
MEDLINE=9425757; PubMed=8199264;
Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;
"Tissue inhibitor of metalloproteinases (TIMP-1) produced by
granulosa and oviduct cells enhances in vitro development of bovine
embryo.";
Biol. Reprod. 50:835-844(1994).
[3]
SEQUENCE OF 25-191 FROM N.A.
TISSUE=Skeletal muscle;
Balcerzak D., Queregeesser L., Dixon W.T., Baracos V.E.;
"Involvement of fibroblasts and muscle cells in the expression of an
extracellular proteolytic cascade in bovine skeletal muscle.";
Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
[4]
PRELIMINARY SEQUENCE OF 24-69.
MEDLINE=90008914; PubMed=2551903;
de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
"Purification and characterization of two related but distinct
metalloproteinase inhibitors secreted by bovine aortic endothelial
cells.";
J. Biol. Chem. 264:17445-17453(1989).
-!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATES THEM.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
-----
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-----
EMBL; J04712; AAA31478.1; -.
PIR; A33350; A33350.
HSSP; P01033; ID2B.
InterPro; IPR001820; TIMP.
Pfam; PF00965; TIMP; 1.
SMART; SM00206; TIMP; 1.
PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 206 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 196 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 188 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 206 AA; 22758 MW; 1839A8DE7174E89E CRC64;
Query Match 87.6%; Score 507; DB 1; Length 206;
Best Local Similarity 86.8%; Pred. No. 4.8e-51;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Best Local Similarity 86.8%; Pred. No. 3.7e-51;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPTEVAQTLLYQRYEIKMTKMYKGFQALGDAADIRF 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 24 CTCVPPHPQTAFNCNSDVVIRAKFVGTAENVETALYQRYEIKMTKMYKGFSAIRDAPDIRF 83
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 VYTPAMESVCGYFRRSHNRSEEFLLIAGKLQDGLLHITTCSFVAPWN 106
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 84 IYTPAMESVCGYFRRSHNRSEEFLLIAGQLSNGHLHITTCSFVAPWN 129
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
TIMP_RABIT
ID TIM1_RABIT STANDARD; PRT; 206 AA.
AC P20614;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214135; PubMed=2708356;
RA Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H.,
RA Quible D.J.;
RT "Hyperoxic exposure alters gene expression in the lung. Induction of
RT the tissue inhibitor of metalloproteinases mRNA and other mRNAs.";
RL J. Biol. Chem. 264:7092-7095(1989).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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CC -----
EMBL; J04712; AAA31478.1; -.
PIR; A33350; A33350.
HSSP; P01033; ID2B.
InterPro; IPR001820; TIMP.
Pfam; PF00965; TIMP; 1.
SMART; SM00206; TIMP; 1.
PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 24 206 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 196 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 188 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 206 AA; 22758 MW; 1839A8DE7174E89E CRC64;
Query Match 87.6%; Score 507; DB 1; Length 206;
Best Local Similarity 86.8%; Pred. No. 4.8e-51;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
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OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPVENQTLVYORYEIKMTKMKYKGFQALGDADIRF 60
 DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPVENQTLVYORYEIKMTKMKYKGFQALGDADIRF 83
 OY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLHITTCSPVAPWN 106
 DB 84 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLHITTCSPVAPWN 129

RESULT 6

TM1L SHEEP STANDARD; PRT; 207 AA.
 ID TM1L SHEEP STANDARD; PRT; 207 AA.
 AC P50122;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 CX NCBI_TaxID=9940;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Corpus luteum;
 RX MEDLINE=94102210; PubMed=8275949;
 RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.;
 RT "Molecular cloning of an ovine ovarian tissue inhibitor of
 RT metalloproteinases: ontogeny of messenger ribonucleic acid expression
 RT and in situ localization within preovulatory follicles and luteal
 RT tissue.";
 RT Endocrinology 134:344-352 (1994).
 RL -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.

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 CC
 CC EMBL; S67450; AAB29472.1; -;
 CC HSSP; P01033; IUEA.
 DR InterPro: IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
 KW Signal.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 FT DISULFID 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 197 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.
 FT DISULFID 168 189 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 207 AA; 23057 MW; 1D3BCA2012F80E46 CRC64;

Query Match 87.0%; Score 504; DB 1; Length 207;
 Best Local Similarity 85.8%; Pred. No. 1,1e-50;
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPVENQTLVYORYEIKMTKMKYKGFQALGDADIRF 60

DB 24 CTCVPHPQTAFCSNDLVIRAKFVGTPVENQTLVYORYEIKMTKMKYKGFQALGDADIRF 83
 OY 61 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLHITTCSPVAPWN 106
 DB 84 VYTPMESVCGYFHRSHNRSEFLIAGKLODGLHITTCSPVAPWN 129

RESULT 7

TM1L PIG STANDARD; PRT; 207 AA.
 ID TM1L PIG STANDARD; PRT; 207 AA.
 AC P35624; Q9TTB3; Q9TTB9;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CX NCBI_TaxID=99823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=92201478; PubMed=1312961;
 RA Tanaka T., Andon N., Takeya T., Sato E.;
 RT "Differential screening of ovarian cDNA libraries detected the
 RT expression of the porcine collagenase inhibitor gene in functional
 RT corpora lutea.";
 RT Mol. Cell. Endocrinol. 83:65-71 (1992).
 RN [2]
 RP SEQUENCE OF 34-195 FROM N.A.
 RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
 RT "Gene expression level of mmp3 and timp1 in interveteral disc.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 37-144 FROM N.A.
 RC TISSUE=Skin;
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine Timp-1.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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 CC
 CC EMBL; S96211; AAB21865.1; -;
 CC EMBL; AF201726; AAF24348.1; -;
 DR EMBL; AF201726; AAF17354.1; -;
 DR HSSP; P01033; IUEA.
 DR InterPro: IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
 KW Signal.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 FT DISULFID 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 197 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.

Query Match 87.0%; Score 504; DB 1; Length 207;
 Best Local Similarity 85.8%; Pred. No. 1,1e-50;
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 OY 1 CTCVPHPQTAFCSNDLVIRAKFVGTPVENQTLVYORYEIKMTKMKYKGFQALGDADIRF 60

CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
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CC -----
DR EMBL; M28312; AAB42179.1; -
DR EMBL; M28308; AAB42179.1; JOINED.
DR EMBL; M28309; AAB42179.1; JOINED.
DR EMBL; M28310; AAB42179.1; JOINED.
DR EMBL; M28311; AAB42179.1; JOINED.
DR EMBL; X04684; CAA28387.1; -
DR EMBL; M17243; AAA40471.1; -
DR PIR; A26633; A26633.
DR PIR; A26106; A26106.
DR HSSP; P01033; 1UBA.
DR MGD; MGI:98752; TIMP.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SMO0206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 205
FT DISULFID 25 94 METALLOPROTEINASE INHIBITOR 1.
FT DISULFID 27 123 BY SIMILARITY.
FT DISULFID 37 148 BY SIMILARITY.
FT DISULFID 151 197 BY SIMILARITY.
FT DISULFID 156 161 BY SIMILARITY.
FT DISULFID 169 189 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 E -> R (IN REF. 1).
FT CARBOHYD 52 66 E -> R (IN REF. 1).
FT CONFLICT 66 66 M -> NM (IN REF. 1).
FT CONFLICT 117 118 N -> KP (IN REF. 1).
FT CONFLICT 121 121 S -> N (IN REF. 1).
FT CONFLICT 139 139 A -> V (IN REF. 1).
FT CONFLICT 143 143 T -> KN (IN REF. 1).
FT CONFLICT 194 194 P -> L (IN REF. 1).
SQ SEQUENCE 205 AA; 22628 MW; 22628 MW; FACA952D49A50FD7 CRC64;
Query Match 79.1%; Score 458; DB 1; Length 205;
Best Local Similarity 74.3%; Pred. No. 2e-45;
Matches 78; Conservative 17; Mismatches 10; Indels 0; Gaps 0;
OY 1 CTCVPHPHQTACNSDLYIRAKFVGTPEVNOTTLVYRREIKMTKWKYKGFALGDADIRF 60
DB 25 CSCAPHPOTACNSDLYIRAKFVGTPEVNOTTLVYRREIKMTKWKYKGFALGDADIRF 84
OY 61 VTPPAMESVCGFHRSHNRSEFLIAGKLODGLHITTCSEFVAPW 105
DB 85 AYTPMESLCGYAKSKQNRSEFLITGRLNGLHISACSEFLVPM 129
RESULT 10
TIM1 CANFA
ID TIM1 CANFA STANDARD; PRT; 207 AA.
AC P81546; Q8T055;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloprotease inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADIN-DUREY;
RA Noritake H., Miyamori H., Goto C., Seiki M., Sato H.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132652; PubMed=9931441;
RA Zeiss C.J., Acland G.M., Aguirre G.D., Ray K.;
RT "TIMP-1 expression is increased in X-linked progressive retinal
RT atrophy despite its exclusion as a candidate gene";
RL Gene 225:67-75(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=92175241; PubMed=1794505;
RA Chopra R., Koklitis P.A., Bergin S., Rowe J., Angal S.;
RT "Purification of recombinant dog tissue inhibitor of
RT metalloproteinases";
RL Biochem. Soc. Trans. 19:372S-372S(1991).
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. HIGHEST IN KIDNEY AND
CC OVARY.
CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
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CC -----
DR EMBL; AB016817; BAA32393.1; -
DR EMBL; AF077817; AAD10632.1; -
DR EMBL; AF079767; AAD10633.1; -
DR HSSP; P01033; 1UBA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SMO0206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1. FALSE NEG.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT SIGNAL 1 23
FT CHAIN 24 207
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 17 17 V -> L (IN REF. 1).
FT CONFLICT 35 35 L -> F (IN REF. 1).
FT CONFLICT 173 173 H -> Q (IN REF. 1).
FT CONFLICT 203 203 MISSING (IN REF. 1).
SQ SEQUENCE 207 AA; 22852 MW; D36C6A67BB3B784D CRC64;
Query Match 78.6%; Score 455; DB 1; Length 207;
Best Local Similarity 78.3%; Pred. No. 4.5e-45;
Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
OY 1 CTCVPHPHQTACNSDLYIRAKFVGTPEVNOTTLVYRREIKMTKWKYKGFALGDADIRF 60
DB 24 CTCAPHPOTACNSDLYIRAKFVGTPEVNOTTLVYRREIKMTKWKYKGFALGDADIRF 83
OY 61 VTPPAMESVCGFHRSHNRSEFLIAGKLODGLHITTCSEFVAPW 106
DB 85 AYTPMESLCGYAKSKQNRSEFLITGRLNGLHISACSEFLVPM 129

Db 84 VDTPAESVCGYLHRSQRSEBFLVAGNLRDGHLQINTCSFVAPWS 129

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RESULT 11
TIM1_RAT
ID TIM1_RAT STANDARD; PRT; 217 AA.
AC P30120; P70533;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1 OR TIMP-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Skin dorsal;
RX MEDLINE=95011636; PubMed=7926820;
RA Okada A., Garnier J.M., Vicaire S., Bassett P.;
RT "Cloning of the cDNA encoding rat tissue inhibitor of
RT metalloproteinase 1 (TIMP-1), amino acid comparison with other TIMPs,
RT and gene expression in rat tissues.";
RL Gene 147:301-302(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Gibbons K.L., O'Grady R.L., Piper A.A.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 30-205 FROM N.A.
RX MEDLINE=96317624; PubMed=8707259;
RA Iredale J.P., Benyon R.C., Arthur M.J.P., Ferris W.F., Alcolado R.,
RA Winwood P.J., Clark N., Murphy G.;
RT "Tissue inhibitor of metalloproteinase-1 messenger RNA expression is
RT enhanced relative to interstitial collagenase messenger RNA in
RT experimental liver injury and fibrosis.";
RL Hepatology 24:176-184(1996).
RN [4]
RP SEQUENCE OF 39-156 FROM N.A., SEQUENCE OF 24-38, INDUCTION, FUNCTION,
RP AND SUBCELLULAR LOCATION.
RC STRAIN=Sprague-Dawley; TISSUE=Sertoli cells;
RX MEDLINE=95296691; PubMed=777858;
RA Boujrad N., Ogwegu S.O., Garnier M., Lee C.-H., Martin B.M.,
RA Papadopoulos V.;
RT "Identification of a stimulator of steroid hormone synthesis isolated
RT from testis.";
RL Science 268:1609-1612(1995).
RN [5]
RP SEQUENCE OF 24-45.
RX MEDLINE=92117648; PubMed=1309971;
RA Roswit W.T., McCourt D.W., Partridge N.C., Jeffrey J.J.;
RT "Purification and sequence analysis of two rat tissue inhibitors of
RT metalloproteinases.";
RL Arch. Biochem. Biophys. 292:402-410(1992).
CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC and irreversibly inactivates them. Also stimulates steroidogenesis
CC by Leydig and ovarian granulosa cells; procathepsin L is required
CC for maximal activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By follicle-stimulating hormone (FSH).
CC -!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
-----
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CC
CC EMBL; U06179; AAA85780.1; -.
DR EMBL; L31883; AAA85373.1; -.
DR EMBL; L29512; AAB08483.1; -.
DR EMBL; U16022; AAA51653.1; ALT_SEQ.
DR PIR; S20326; S20326.
DR HSP; P01033; IUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
KW Steroidogenesis; Signal.
FT SIGNAL 1 23
FT CHAIN 24 217
FT DISULFID 24 93
FT DISULFID 26 122
FT DISULFID 36 147
FT DISULFID 150 197
FT DISULFID 155 160
FT DISULFID 168 189
FT CARBOHYD 77 77
FT CARBOHYD 101 101
FT CONFLICT 80 81
FT CONFLICT 88 88
FT CONFLICT 103 103
FT CONFLICT 129 130
FT CONFLICT 136 140
FT CONFLICT 149 149
FT CONFLICT 157 157
FT CONFLICT 166 166
FT CONFLICT 185 187
FT CONFLICT 195 195
FT CONFLICT 201 201
FT CONFLICT 204 205
SQ SEQUENCE 217 AA; 23793 MW; C5AC240A61C1AIDF CRC64;
Query Match 77.0%; Score 446; DB 1; Length 217;
Best Local Similarity 73.6%; Pred. No. 5.2e-44;
Matches 78; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
Oy 1 CTCVPPHQTAFCSNLDVIRAKFVGTPEVNTQTLVQRIKMTYKGFQALGDAADIRF 60
Db 24 CSCAPTHPTAFCSNLDVIRAKFMGSPETITLYQRIEIKTKLKGFDVGNATGRF 83
Oy 61 VYTPAMESVCCGYFHRSNRSSEFLIAGKLQDGLLHITTCSPVAPWN 106
Db 84 AYTPAMESLCGYVHKSNRSSEFLIAGLRLNGNLHITACSLVPPWH 129
RESULT 12
TIM3_SCYTO
ID TIM3_SCYTO STANDARD; PRT; 214 AA.
AC Q9W6B4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metalloproteinase inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of
DE metalloproteinases-3).
GN TIMP3.
OS Scyliorhinus torazame (Cloudy catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=75743;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX PubMed=11342115;
RA Kim J.T., Kim M.-S., Bae M.-K., Ahn M.-Y., Kim Y.-J.,
RA Lee S.-J., Kim K.-W.;
RT "Cloning and characterization of tissue inhibitor of
```

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RT metalloproteinase-3 (TIMP-3) from shark, Scyliorhinus torazame." ;
RL Biochim. Biophys. Acta 1517:311-315(2001).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM. MAY FORM PART OF A TISSUE-
CC SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain and cartilage.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
-----
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-----
CC EMBL, AF110767; AAD26150.1; -.
CC HSSP, P16035; 2TMP.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP.1.
DR SMART, SM00206; TIMP.1.
DR PROSITE, PS00288; TIMP.1.
KW Metalloprotease inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 27 214 METALLOPROTEINASE INHIBITOR 3.
FT DISULFID 27 94 BY SIMILARITY.
FT DISULFID 29 121 BY SIMILARITY.
FT DISULFID 39 146 BY SIMILARITY.
FT DISULFID 148 195 BY SIMILARITY.
FT DISULFID 153 158 BY SIMILARITY.
FT DISULFID 166 187 BY SIMILARITY.
FT CARBOHYD 210 210 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 214 AA; 2499 MW; BCAD300B8E483557 CRC64;

Query Match 40.6%; Score 235; DB 1; Length 214;
Best Local Similarity 43.0%; Pred. No. 9.2e-20;
Matches 46; Conservative 19; Mismatches 36; Indels 6; Gaps 3;

OY 1 CTCVPHPQTACNSDVIYRAKFGVTPVNOQTL-YQRYEIKTKMYKGFQALGDAADIR 59
DB 27 CTCMHNHPQEARCNSDIVIRAKVKGKLLKDGPFMTGRYTIKQMKMYRGFSKM---QQVQ 83
OY 60 FVYTPAMESVCGYFHRSHRSEFLIAGLQDGLHTTCGFPAPMN 106
DB 84 YIYTRAEBSLGGV--RLQYNKFQYLITGRVFDGEVYTVGVCFIVPWD 128

RESULT 13
TIM2_HUMAN STANDARD; PRT; 220 AA.
AC Q9WOC6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2).
GN TIMP2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RX MEDLINE=20215260; PubMed=10749751;
RA Melendez J., Maldonado V., Selman M., Pardo A.;
RT "Cloning and expression of guinea pig TIMP-2. Expression in normal and
RT hyperoxic lung injury."
RL Am. J. Physiol. 278:L737-L743(2000).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM.
```

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LUNG IN
CC ALVEOLAR MACROPHAGES AND EPITHELIAL CELLS. ALSO FOUND IN BRAIN,
CC KIDNEY, INTESTINE, SPLEEN, AND HEART.
CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE TIMP FAMILY.
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-----
CC EMBL, AF127803; AAD28252.1; -.
CC HSSP, P16035; 1BR9.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP.1.
DR SMART, SM00206; TIMP.1.
DR PROSITE, PS00288; TIMP.1.
KW Metalloprotease inhibitor; Signal.
FT SIGNAL 1 26
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 27 98 BY SIMILARITY.
FT DISULFID 29 127 BY SIMILARITY.
FT DISULFID 39 152 BY SIMILARITY.
FT DISULFID 154 201 BY SIMILARITY.
FT DISULFID 159 164 BY SIMILARITY.
FT DISULFID 172 193 BY SIMILARITY.
SQ SEQUENCE 220 AA; 24318 MW; 2A2541764755B9AF CRC64;

Query Match 40.4%; Score 234; DB 1; Length 220;
Best Local Similarity 44.7%; Pred. No. 1.2e-19;
Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

OY 1 CTCVPHPQTACNSDVIYRAKFGVTPVNO-TTLYO-----RYEIKTKMYKGFQALG 53
DB 27 CSCSPVHPQAFCSNDIVIRAKAVSEKEDVSGNDIYGNPIKRIQYIKQIKMFK-----G 81
OY 54 DADIRFVYTPAMESVCGYFHRSHRSEFLIAGLQ-DGLHTTCGFPAPMN 106
DB 82 PKDIEFIYITASAVCG-VSLDVGKKEKYLIAKAEKDGKMHITLCPIVPWD 134

RESULT 14
TIM2_HUMAN STANDARD; PRT; 220 AA.
AC P16035; Q93006; Q16121; Q9UDF7;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2) (CSC-21K).
GN TIMP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2380196; PubMed=2380196;
RA Stetler-Stevenson W.G., Brown P.D., Onisto M., Levy A.T., Liotta L.A.;
RT "Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA expression in
RT tumor cell lines and human tumor tissues."
RL J. Biol. Chem. 265:13933-13938(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90207285; PubMed=2157214;
RA Boone T.C., Johnson M.J., de Clerck Y.A., Langley K.E.;
RT "cDNA cloning and expression of a metalloproteinase inhibitor related
RT to tissue inhibitor of metalloproteinases." ;
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Db 82 PEKDIFFIYAPSSAVCG-VSLDVGKKEYLIAGKAGDGKWHITLCDPIVPMW 134

RESULT 15

TIM2_CRIL0 STANDARD; PRT; 196 AA.
AC Q60453;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
DE metalloproteinases-2) (Fragment).
GN TIMP2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OS Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus
OK NCBI_TaxID=10030;
PR (1)
PR SEQUENCE FROM N.A.
RA Tissue=Ovary;
RA Suzuki Y.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATES THEM (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE TIMP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X75924; CAA53528.1; -
CC HSSP: P16035; 1BR9.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Metalloproteinase inhibitor; Signal.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 1 2 BY SIMILARITY.
FT DISULFID 3 196 METALLOPROTEINASE INHIBITOR 2.
FT DISULFID 3 74 BY SIMILARITY.
FT DISULFID 5 103 BY SIMILARITY.
FT DISULFID 15 128 BY SIMILARITY.
FT DISULFID 130 177 BY SIMILARITY.
FT DISULFID 135 140 BY SIMILARITY.
FT DISULFID 148 169 BY SIMILARITY.
SQ SEQUENCE 196 AA; 21941 MW; 2ADAB9B54AF75381 CRC64;

Query Match 40.2%; Score 233; DB 1; Length 196;
Best Local Similarity 44.7%; Pred. No. 14e-19;
Matches 51; Conservative 15; Mismatches 34; Indels 14; Gaps 5;

QY 1 CTCVPPHPQTAFCSNLDVIRAKFVGTPENVQ--TTLYQ-----RYEIKMTKMYKGFQALG 53
Db 3 CSCSPVHPQOACNDVIRAKAVSEKVDGNDIYGNPIKRIQYFIKQIKMF-----G 57
QY 54 DAADIRFVYTPMESVYCYFHRSHNRSEFLIAGKIQ-DGLIHITTCGTFVAPWN 106
Db 58 PKDKIEFIYAPSSAVCG-VSLDVGKKEYLIAGKAGDGKWHITLCDPIVPMW 110

Search completed: December 17, 2002, 15:04:52
Job time : 5.84828 secs

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OM protein - protein search, using sw model

Run on: December 17, 2002, 15:04:31 ; Search time 19.3724 Seconds
(without alignments)
1127.428 Million cell updates/sec

Title: US-09-452-817-2

Perfect score: 579
Sequence: 1 CTCVPPHPQTAFNCNSDLVIR.....GKLDPGLHITTCFVAPWN 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	579	100.0	169 4 Q96QM2	Q96QM2 homo sapien
2	463	80.0	137 6 Q9M212	Q9M212 ovis aries
3	222	38.3	194 11 Q925Q6	Q925Q6 mesocricetu
4	219	37.8	145 11 Q912P7	Q912P7 rattus norv
5	165	28.5	126 6 Q95KL7	Q95KL7 macaca mula
6	159	27.5	152 6 Q9RTB7	Q9RTB7 sus scrofa
7	153	26.4	138 6 Q9RTB8	Q9RTB8 sus scrofa
8	143.5	22.8	170 6 Q9RTB6	Q9RTB6 sus scrofa
9	129.5	22.4	97 13 Q8U22	Q8U22 xenopus lae
10	124	21.4	25 11 Q9QUW9	Q9QUW9 rattus sp.
11	124	21.4	25 11 Q9QV13	Q9QV13 mus sp. col
12	111.5	19.3	221 5 Q9GBJ2	Q9GBJ2 crassostrea
13	106	18.3	30 11 Q9QV14	Q9QV14 mus sp. col
14	83.5	14.4	187 5 Q9NDF1	Q9NDF1 heterodera
15	75.5	13.0	257 16 Q932H6	Q932H6 staphylococ
16	75.5	13.0	1106 13 Q42291	Q42291 gallus gall

17	74	12.8	158 5 Q21265	Q21265 caenorhabdi
18	72	12.4	530 10 Q80793	Q80793 arabidopsis
19	70.5	12.2	122 11 Q8R3X3	Q8R3X3 mus musculu
20	70	12.1	1118 10 Q93VL6	Q93VL6 phaseolus v
21	69	11.9	345 11 Q9CV42	Q9CV42 mus musculu
22	68	11.7	388 16 Q98B78	Q98B78 rhizobium l
23	68	11.7	902 11 Q9DBK8	Q9DBK8 mus musculu
24	68	11.7	941 11 Q91W60	Q91W60 mus musculu
25	68	11.7	942 11 Q54882	Q54882 mus musculu
26	67.5	11.7	2328 6 Q95M19	Q95M19 erinaceus e
27	66.5	11.5	490 16 Q9HTJ1	Q9HTJ1 pseudomonas
28	66	11.4	597 16 Q9P9N3	Q9P9N3 xylella las
29	65.5	11.3	220 2 Q9XBQ4	Q9XBQ4 bacillus st
30	65.5	11.3	517 4 Q75294	Q75294 homo sapien
31	65	11.2	161 11 Q9CSF1	Q9CSF1 mus musculu
32	65	11.2	943 10 Q94CU5	Q94CU5 oryza sativ
33	64.5	11.1	195 16 Q9ZEP0	Q9ZEP0 listeria in
34	64.5	11.1	853 5 Q8T4K1	Q8T4K1 dictyosteli
35	64.5	11.1	923 5 Q9N506	Q9N506 caenorhabdi
36	64	11.1	46 11 Q8VH23	Q8VH23 mus musculu
37	64	11.1	932 11 Q35802	Q35802 rattus norv
38	64	11.1	995 4 Q9NRZ1	Q9NRZ1 homo sapien
39	64	11.1	1035 4 Q15153	Q15153 homo sapien
40	64	11.1	1079 4 Q9Y6R1	Q9Y6R1 homo sapien
41	64	11.1	1079 4 Q9UIC0	Q9UIC0 homo sapien
42	64	11.1	1079 4 Q9UP50	Q9UP50 homo sapien
43	64	11.1	1079 4 Q9H262	Q9H262 homo sapien
44	63.5	11.0	457 3 Q9C1W3	Q9C1W3 schizosach
45	63	10.9	387 10 Q9M9V1	Q9M9V1 arabidopsis

ALIGNMENTS

RESULT 1				
Q96QM2	PRELIMINARY:	PRT:	169 AA.	
ID	Q96QM2			
AC	Q96QM2;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Tissue inhibitor of metalloproteinase 1 (erythroid potentiating			
DE	activity, collagenase inhibitor).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Butcheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PROSTATE;			
RA	Straussberg R.;			
RL	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC007097; AA07097.1; -.			
DR	InterPro; IPR001820; TIMP.			
DR	Pfam; PF00965; TIMP. 1.			
DR	PROSITE; PS00288; TIMP; UNKNOWN 1.			
SQ	SEQUENCE 169 AA; 18847 MM; 6C164206C87D815C CAC64;			
Query Match	100.0%; Score 579; DB 4; Length 169;			
Best Local Similarity	100.0%; Pred. No. 1.8e-59;			
Matches 106; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 CTCVPPHPQTAFNCNSDLVIRAKFVGTPVNOYLYORREIKTKYKGOALGDADIRF 60			
DB	24 CTCVPPHPQTAFNCNSDLVIRAFVGTPEVNOYLYORREIKTKYKGOALGDADIRF 83			
QY	61 VTTPMESVCGYFHRSHNRSEFLIAGKLDGLHITTCFVAPWN 106			
DB	84 VTTPMESVCGYFHRSHNRSEFLIAGKLDGLHITTCFVAPWN 129			
RESULT 2				
Q9M212				

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ID Q9MZ12 PRELIMINARY; PRT; 137 AA.
AC Q9MZ12;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347710; PubMed=10898873;
RA Galloway S.M., McNatty K.P., Cambridge L.M., Laitinen M.P.E.,
RA Juengel J.L., Jokiranta S., McLaren R.J., Luiro K., Dodds K.D.,
RA Montgomery G.W., Beattie A.E., Davis G.H., Ritvos O.;
RT "Mutations in an oocyte-derived growth factor (BMP15) cause increased
RT ovulation rate and infertility in a dosage-sensitive manner.";
RL Nat. Genet. 25:279-283(2000).
DR EMBL; AF268477; AAF81746.1; -.
DR HSSP; P01033; 1D2B.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; TIMP; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15396 MW; 62009B069D0594B7 CRC64;

Query Match 80.0%; Score 463; DB 6; Length 137;
Best Local Similarity 85.0%; Pred. No. 4.5e-46;
Matches 85; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 7 HPQTAFNCNSDLVIRAKFVGTPEVNOTTYQRYEIKWTMYKGFQALGDAAADIRFVYTPAM 66
Db 1 HPQTAFNCNSDLVIRAKFVGTPEVNOTTYQRYEIKWTMYKGFQALGDAAADIRFVYTPAM 60

Qy 67 ESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSFVAPWN 106
Db 61 ESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSFVAPWN 100

RESULT 3
Q925Q6 PRELIMINARY; PRT; 194 AA.
AC Q925Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-2 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX KO K.H., Shin C.Y., Lee W.J., Yoo B.K., Ryu J.R., Park K.H.;
RT "Expression of metalloproteinase-2 (gelatinase A) and tissue inhibitor
RT of metalloproteinase-2 (TIMP-2) from hamster tracheal goblet cells: a
RT possible role in upper airway inflammation.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260255; AAK51636.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 194
SQ SEQUENCE 194 AA; 21763 MW; 1C5D10A3038A8941 CRC64;

Query Match 38.3%; Score 222; DB 11; Length 194;
Best Local Similarity 43.0%; Pred. No. 7.8e-18;
Matches 49; Conservative 16; Mismatches 35; Indels 14; Gaps 5;

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Qy 1 CTCVPPHPOTAFNCNSDLVIRAKFVGTPEVNOQ-TTLYQ-----RYEIKWTMYKGFQALG 53
Db 1 CSCSPVHQQAFCNADVVIRAKAVSEKVDGNDIYGNPVKRIQYIKRMFX-----G 55

Qy 54 DAAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSFVAPWN 106
Db 56 PKDIEFIYAPSSAMCG-VSLDVGKGKEYLIAGKAGDGKMHITLCDFIVPND 108

RESULT 4
Q91ZP7 PRELIMINARY; PRT; 145 AA.
AC Q91ZP7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WISTAR; TISSUE-OVARY;
RA Espey L.L., Ujioka T., Okamura H., Richards J.S.;
RT "Expression of metallothionein-1 (MT-1) in steroid-secreting cells of
RT the rat ovary during the peri-ovulatory period following gonadotropin
RT treatment.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411319; AAL05862.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15954 MW; 7EC7053DA82DE913 CRC64;

Query Match 37.8%; Score 219; DB 11; Length 145;
Best Local Similarity 67.9%; Pred. No. 1.2e-17;
Matches 38; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 51 ALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGKLDGLLHITTCSFVAPWN 106
Db 2 AVGNATGFRFAYTPAMESLCGYVHKSQNRSEEFLLAGLRNGLNHLITACSLVLPWH 57

RESULT 5
Q95KL7 PRELIMINARY; PRT; 126 AA.
AC Q95KL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tissue inhibitor of matrix metalloproteinase-3 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX JI S., Wang Y., Li H., Ji W., Piao Y.;
RT "Cloning and characterization of tissue inhibitor of matrix
RT metalloproteinase-3 (TIMP-3) cDNA from Macaca mulatta.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366399; AAK53706.1; -.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 14690 MW; 2F162249A7D2615E CRC64;

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Query Match 28.5%; Score 165; DB 6; Length 126;
 Best Local Similarity 37.8%; Pred. No. 2e-11;
 Matches 37; Conservative 20; Mismatches 31; Indels 10; Gaps 4;

OY 12 FNSDLVIRAKVGVPEVNO---TTLQRYEIKMTKMYGFOALGDAADIRFVYTPAMESV 68
 DB 1 FNSDLVIRAKVGVKLVVEGPGFTLV--YTIKMKMYRGFTKM--PHVQYHTEASES 55

OY 69 VCGFHRSHNRSEEFLLAGKLDGLHITTCSPVAPWN 106
 DB 56 LCGL--KLEVNKYQYLLTGRVYDGKMYTGLCNFVERWD 91

RESULT 6
 OYTB7 PRELIMINARY; PRT; 152 AA.

ID OYTB7
 AC OYTB7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Metalloprotease inhibitor 3 (TIMP-3) (Tissue inhibitor of metalloproteinases-3) (Fragment).

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs."
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 RL FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM. MAY FORM PART OF A TISSUE-SPECIFIC ACUTE RESPONSE TO REMODELING STIMULI.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 CC EMBL; AF156031; AAF17356.1; --
 CC HSSP; P16035; 1BR9.
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR KX Metalloprotease inhibitor.

FT NON_TER 1 1
 FT DISULFID 2 109 BY SIMILARITY.
 FT DISULFID 116 121 BY SIMILARITY.
 FT DISULFID 129 150 BY SIMILARITY.
 FT NON_TER 152 152
 GN SEQUENCE 152 AA; 17736 MW; 4050E5F5FC58B5E7 CRC64;

Query Match 27.5%; Score 159; DB 6; Length 152;
 Best Local Similarity 37.1%; Pred. No. 1.3e-10;
 Matches 36; Conservative 20; Mismatches 31; Indels 10; Gaps 4;

OY 13 CNSDLVIRAKVGVPEVNO---TTLQRYEIKMTKMYGFOALGDAADIRFVYTPAMESV 69
 DB 2 CNSDLVIRAKVGVKLVVEGPGFTLV--YTIKMKMYRGFTKM--PHVQYHTEASES 56

OY 70 CGFHRSHNRSEEFLLAGKLDGLHITTCSPVAPWN 106
 DB 57 CGL--KLEVNKYQYLLTGRVYDGKMYTGLCNFVERWD 91

RESULT 7
 OYTB8 PRELIMINARY; PRT; 138 AA.

ID OYTB8
 AC OYTB8
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Metalloprotease inhibitor 2 (TIMP-2) (Tissue inhibitor of metalloproteinases-2) (Fragment).

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs."
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 RL FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 CC EMBL; AF156032; AAF17357.1; --
 CC HSSP; P16035; 2TMP.
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR KX Metalloprotease inhibitor.

FT NON_TER 1 1
 FT DISULFID 107 154 BY SIMILARITY.
 FT DISULFID 112 117 BY SIMILARITY.
 FT DISULFID 125 146 BY SIMILARITY.
 FT NON_TER 170 170

Query Match 26.4%; Score 153; DB 6; Length 138;
 Best Local Similarity 39.8%; Pred. No. 5.6e-10;
 Matches 39; Conservative 13; Mismatches 32; Indels 14; Gaps 5;

OY 17 LVIRAKVGVTPPEVNO-TTLQYQ-----RYEIKMTKMYGFOALGDAADIRFVYTPAMESV 69
 DB 1 VVIRAKVSEKVDGNDIYGNPIRIQYIEIKQIMFK-----GPKDIEFYTPSSAV 55

OY 70 CGFHRSHNRSEEFLLAGKLDGLHITTCSPVAPWN 106
 DB 56 CG-VSLDIGKKKYYLIAGKAGHGHHITLCPFIVPW 92

RESULT 8
 OYTB6 PRELIMINARY; PRT; 170 AA.

ID OYTB6
 AC OYTB6
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Metalloprotease inhibitor 4 (TIMP-4) (Tissue inhibitor of metalloproteinases-4) (Fragment).

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs."
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 RL FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREVERSIBLY INACTIVATES THEM.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.
 CC EMBL; AF156032; AAF17357.1; --
 CC HSSP; P16035; 2TMP.
 DR InterPro; IPR001820; TIMP.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; TIMP; 1.
 DR KX Metalloprotease inhibitor.

FT NON_TER 1 1
 FT DISULFID 107 154 BY SIMILARITY.
 FT DISULFID 112 117 BY SIMILARITY.
 FT DISULFID 125 146 BY SIMILARITY.
 FT NON_TER 170 170

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DR HSSP; P01033; lUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00288; TIMP; 1.
DR SQ SEQUENCE 25 AA; 2698 MW; 35129B2B74C1FDAF CRC64;

Query Match      21.4%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. NO. 1.8e-07;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCVPPHPQTAFCNSDLIVIRAKFWG 25
    :|:|||||||
Db 1 CSCAPTHPTAFCNSDLIVIRAKFWG 25
    :|:|||||||

RESULT 11
Q9QV13 PRELIMINARY; PRT; 25 AA.
AC Q9QV13;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Collagenase inhibitor MS-31 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE
RX MEDLINE=95105266; PubMed=7806596;
RA Rosenthal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,
RA Folkman J.;
RT "Purification and characterization of two collagenase inhibitors from
RT mouse sarcoma 180 conditioned medium.";
RL J. Cell. Biochem. 56:97-105(1994).
DR HSSP; P01033; lUEA.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SQ SEQUENCE 25 AA; 2678 MW; 923226E82C1901FD CRC64;

Query Match      21.4%; Score 124; DB 11; Length 25;
Best Local Similarity 84.0%; Pred. NO. 1.8e-07;
Matches 21; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCVPPHPQTAFCNSDLIVIRKFGVT 26
    :|:|||||||
Db 1 SCAPPHPQTAFCNSDLIVIRKFGWS 25
    :|:|||||||

RESULT 12
Q9GPJ2 PRELIMINARY; PRT; 221 AA.
AC Q9GPJ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tissue inhibitor of metalloproteinase TIMP.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostroidea; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21329024; PubMed=11434928;
RA Montagnani C., Le Roux F., Berthe F., Escoubas J.M.;
RT "Cg-TIMP, an inducible tissue inhibitor of metalloproteinase from the
RT Pacific oyster Crassostrea gigas with a potential role in wound
RT healing and defense mechanisms.";
RL FEBS Lett. 500:64-70(2001).
DR ENBL; AF321279; XAG42824.1; -.
DR HSSP; Pf6035; IIR9.
DR InterPro; IPR001820; TIMP.
DR Pfam; PF00965; TIMP; 1.

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DR SMART; SM00206; TIMP; 1.
SQ SEQUENCE 221 AA; 25332 MW; AAS3F67EB137A06A CRC64;

Query Match 19.3%; Score 111.5; DB 5; Length 221;
Best Local Similarity 27.5%; Pred. No. 6.7e-05;
Matches 33; Conservative 19; Mismatches 41; Indels 27; Gaps 6;

QY 1 CTCVPPHPQTAFCONSGLVIRAKFV-----GTP---EVNQTLLYQRYEIKMTKMY 46
DB 23 CMCDFTHPNNKCSADPVIKATIVKELKFGDSKMGIPFLQKNYVQPKKDI-----F 77
QY 47 KCPQALGDAADIRFYVTPMSEVCGYFHRSHNRSEFLIAGLQDGLHITTCSEVAPWN 106
DB 78 KSSSLIG--SDTLVKTSGTQPMNCG---ETFLINKKEYVISGFVSDGEFTNNCQ---WN 129

RESULT 13
Q9QV14 PRELIMINARY; PRT; 30 AA.

Q9QV14; 09QV14;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Collagenase inhibitor MS-22 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10095;

RA MEDLINE=95105266; PubMed=7806596;
RA Rosenthal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,
RA Folkman J.;
RT "Purification and characterization of two collagenase inhibitors from
RT mouse sarcoma 180 conditioned medium.";
RL J. Cell. Biochem. 56:97-105(1994).
DR HSP; P16035; IBR9.
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.
DR PROSITE: PS00288; TIMP; 1.
SQ SEQUENCE 30 AA; 3232 MW; EB658F11186284D9 CRC64;

Query Match 18.3%; Score 106; DB 11; Length 30;
Best Local Similarity 63.3%; Pred. No. 2.7e-05;
Matches 19; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

1 CTCVPPHPQTAFCONSGLVIRAKFVGTPEVN 30
1 CSQSPVHPQAFQCNADVIRAKAVSEKVD 30

RESULT 14

Q9NDF1 PRELIMINARY; PRT; 187 AA.

Q9NDF1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical esophageal gland cell secretory protein 12.
GN HSP12.
OS Heterodera glycines (Soybean cyst nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=51029;

RA SEQUENCE FROM N.A.
RA Wang X., Ding X., Maier T., Goellner M., Baum T.J., Hussey R.S.,
RA Davis E.L.;
RT "Nematode metalloproteinase inhibitor precursor";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159591; AAF76926.1; -
DR InterPro: IPR001820; TIMP.
DR Pfam: PF00965; TIMP; 1.

DR SMART; SM00206; TIMP; 1.
SQ SEQUENCE 187 AA; 21450 MW; C171A2589B8824D8 CRC64;

Query Match 14.4%; Score 83.5; DB 5; Length 187;
Best Local Similarity 23.0%; Pred. No. 0.1;
Matches 26; Conservative 20; Mismatches 50; Indels 17; Gaps 3;

QY 1 CTCVPPHPQTAFCONSGLVIRAKFVGTPE-----VNQTTLYQRYEIKMTKMYKGFQA 51
DB 38 CQQAAPPKDNVNCSSDWAHVAVQIRKQGVMPAGITRQDTLNSRHEKYLARMKISKQ 97
QY 52 LCDADIRF---VTPMSEVCGYFHRSHNRSEFLIAGLQDGLHITTC 99
DB 98 MEVNOONQVILIPVNYTATEDAACGILLES---GHQYLLAGDGVNAGTMTGLC 147

RESULT 15
Q932H6 PRELIMINARY; PRT; 257 AA.

Q932H6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein SAV0410.
GN SAV0410.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878;

RA MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K., I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanemori M., Matsumaru H., Murayama A., Murakami H., Hosoyama A.,
RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake S. K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003359; BAB56572.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 30671 MW; FEBD7041A94BEE3 CRC64;

Query Match 13.0%; Score 75.5; DB 16; Length 257;
Best Local Similarity 28.8%; Pred. No. 1.2;
Matches 23; Conservative 11; Mismatches 25; Indels 21; Gaps 3;

QY 8 POTAFCONSGLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALG-----DAADIRF 60
DB 66 PSSSLQTTDYLEIGKMCFLPEMNQTN-----YFQSQALSALIKWLKEHTDCHF 113

QY 61 VYTPA--MESVCGYFHRSHN 78
DB 114 LYTLADGIEGKCGYVQASN 133

Search completed: December 17, 2002, 15:08:10
Job time : 20.3724 secs

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